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OM nucleic - nucleic search, using sw model

November 21, 2004, 20:12:11; Search time 22705 Seconds (without alignments) 11657.364 Million cell updates/sec Run on:

US-10-023-888-3 5597 1 cggagccgagcggcgtccg.....aaaaagttaaattttgaaaa 5597 Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4526729 seqs, 23644849745 residues Searched:

9053458

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Genmahl: \*

1: 90 ba: \*

1: 90 ba: \*

1: 90 ow: \*

1: 90 ow: \*

2: 90 pr: \*

2: 90 pr: \*

3: 90 pr: \*

3: 90 pr: \*

4: 90 pr: \*

5: 90 pr: \*

6: 90 pr: \* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				
CN	Score	Match	Length	DB	ID	Description
	5597	100.0	5597	9	AR300462	AR300462 Sequence
7	5597	100.0	5597	9	AR428739	AR428739 Sequence
m	5597	100.0	5597	9	AR442828	AR442828 Sequence
4	4475.2	80.0	4511	σ	AB033034	AB033034 Homo sapi
Ŋ	4326	77.3	4369	9	AX468102	AX468102 Sequence
9	4057	72.5	4277	9	AX468106	AX468106 Sequence
7	3761	67.2	3783	9	AR300471	AR300471 Sequence
œ	3761	67.2	3783	9	AR428748	AR428748 Sequence
σ	3761	67.2	3783	9	AR442837	AR442837 Seguence
10	3485.4	62.3	3621	ø	AR300472	AR300472 Sequence
11	3485.4	62.3	3621	9	AR428749	AR428749 Sequence
12	3485.4	62.3	3621	9	AR442838	AR442838 Sequence
13	3100.2	55.4	3150	σ	BC042615	BC042615 Homo sapi
14	2874.6	51.4	5204	10	AK173132	AK173132 Mus muscu
15	2820.8	50.4	5229	φ	AR300468	AR300468 Sequence
16	2820.8	50.4	5229	ø	AR428745	AR428745 Sequence
17	2820.8	50.4	5229	v	AR442834	AR442834 Sequence
18	2755.8	49.2	3152	9	CQ719596	CQ719596 Sequence
19	2587.4	46.2	2603	ø	AX714069	AX714069 Sequence

	BD176860 A method	AL359588 Homo sapi		Prime	AK001821 Homo sapi	BC060638 Mus muscu	AC063950 Homo sapi	AC005409 Homo sapi	BC071687 Homo sapi	ø	CQ067110 Sequence	CQ094163 Sequence	7	S	S)	ro co	8	6	01	51	CQ341629 Sequence	L36434 Mus Musculu	AX806612 Sequence	13	BD149281 Primer fo
AK056137	5 BD176860		5 AX877611	6 BD156750	9 AK001821	0	_	3 AC005409	_	5 CQ052066									-	10	5 CQ341629	10 MUSBDLZ	5 AX806612	5 AX869219	5 BD149281
2603	2428	2428	2076	2076	2076	4699	174231	177364	1718	1962	1962	1962	1962	1962	1962	1125	1125	1125	1125	1125	1125	1846	728	780	78
46.2	42.4	42.4		36.1	36.1	32.1	30.7	30.7	27.6	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	19.7	15.5	12.9	12.4	12.4
2587.4	2372.2	ന	2018.2		2018.2	1795.4	1716.4	1716.4	1544.2	1104.8	1104.8	1104.8	1104.8	1104.8	1104.8	1103.4	1103.4	1103.4	1103.4	1103.4	1103.4	869		692	O.
20			23			26	'n	~	29	30	m	32	m	34	m	36	'n	m	c 39	4	4,	42	43	44	45

## ALIGNMENTS

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GAGATCAATACCATGATTTGATTCCAATTCCAATTCGAACAGGATTTTGGAAGCCTTCTTCTAGAAGACATAATTGCAAGCCTTTCTAGAAGACAATAATTGCAAGACAATAATTGCAATAATAATAATAATAATAATAATAATAATAATAATAAT	à a	1381 AIGAIGAIGAIGAITINGGGAAGAIGACTGGCCAGAIGAITTTTACAGTCACTCCAAAG 1440 
GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 36 AGAATCGGCTTTGTCTGCCCATGCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG 42	\$ a	1441 GCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAGGGCTGCCCAGGTTCCT 1500
AGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG 42 ATCTTGAACTACTGAAGGAACTACAGCAGGAGGAGGAAGGA	\$ A	1501 GGATTAAGGATGGCTATTGTGACAAGGCTTGTAATAATTCAGCCTGCGATTGGGATGGTG 1560
ATCTTGAACTACTGAAGGAACTACAGCAGGTCAGAGAACAGATGGAGGAGGAGGAGGAGAAGAAGAAGAAGCAACAAAGAAAGAAG	ò da	1561   GGGATTGCTCTGGAAACAGTGGAGGGAGTCGCTATATTGCAGGAGGTGGAGGTACTGGGA 1620 
981 CARIGAGAGARATICCIIGGGARAAACACAACGAACCIACIAAGAAGAGGAGGGAGAGGGAGAGGGAGAGGGAGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGA	\$ g	1621 GTATTGGAGTTGGACACCCTGGCAGTTTGGTGGAGGAATAAACAGTGTCTTACTGTA 1680 
CAGCCAACATCACCCTGAAGGACGTGCCATCTTTAATCCTTTTTCATTCTGCCAGTG 6	ò 8	1681 ATCAGGGATGTGCGAATTCCTGGCTGGCTGATAAGTTCTGTGACCAAGCATGCAATGTT 1740 
ACATTICAATGITGCAAAGGACGIGCCAICICIIIAICCIICIIIICIGCCAGIG 8 ACATTITCAATGITGCAAAACGAAAAACCCTICTACCAATGICTCAGITGITTITT 7	ò a	1741 TGTCCTGTGGGTTTGATGCTGGGGGCTGTGGGGCAAGATCATTTTCATGAATTGTATAAAG 1800 
ACAGTACTAAAGGATGTTGAAAAACCCATCTGTACCAATGTGTCTCAGTTGTTTTTG 72 ACAGTACTAAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGACAGA	<i>장</i> 쉼	1801 TGATCCTTCTCCCAAACCAGACTCACTATATTATTCCAAAAGGTGAATGCCTGCC
ACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGACAGA	& 8	1861 TCAGCTTTGCAGAAGTAGCCAAAAGGAGGAGTGCAGGGCCCTATAGTGACAATCAAT
CAGTATGGAGGGGGGTACTTGACACAGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAG. 84 ATTTGGCTTTCCTGAGTTGCACCAACATCAAGGAAACAATCAACTAAAAACAA 90	\$ 8 8	1921 TTCGACATGCTTCTATTGCCAACAGTGGAAAACCATCCACCTCATAATGCACAGTGGAA 1980 
ALTIGGETTICETGAGIGGATTTCCACCAACATTCAAGGAAACAAATCAACIAAAAACAA 90 AATIGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTGTATCAGAGGCCAGTG 96	, & 43	1981 TGARTGCCACCACAATACATTTTAATCTCACGTTTCAAAATACAAACGATGAAGAGTTCA 2040 
AATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCCAGTG TAGCGCTTCTAAAACTGAATACCCCAAGGATTTTCAAGAATTGAATAAGAACTAAGA	ζς, Gp	2041 AAATGCAGATRACAGTGGAGGTGGACACAAGGGAGCAAAACTGAATTCTACGGCCC 2100 2041 AAATGCAGATAACAGTGGAGGTGGACAAAGGGAGGAGGACCAAAACTGAATTCTACGGCCC 2100
AGAACATGATAGAAGAAAAAAAAAAAAAAAAAAAAAAAA	8 %	2101 AGAAGGGTACGAAAATTAGTTAGTCCCATAACACTTCTTCCAGAGGCGGAAATCCTT 2160 
AGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATATGGGATTC 108 TGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGAACATCTCTGCCAGTCGTTTTGAAGATA 114	& 8	2161 TTGAGGATATTCCCAAAGAAAAGGCTTCCCGAAGTTTAAGAGACATGATGTTAACTCAA 2220 
TGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAAGATA 114 ACGAAGAACTAACGATGCGATCTATCGAGAGGCATGCACCATGGGTTCGGAATA 120	& 8	2221 CAAGGAGCCCAGGAAGAGGGGAAAATTCCCCTGGTAAATATTTCACTCCTTCCAAAAG 2280 
ACGAAGAACTGAGGTACTCATTGCGATCTATCGAGAGGCATGCACCATGGGTTCGGAATA 120 TTTTCATTGTCACCAACGGGCAGATTCCATCGTGGCTGAACCTTGACAATCCTCGAGTGA 126	6 6	2281 ACGCCCAGTIGAGICTCAAIACCTIGGAITIGCAACIGGAACAIGGAGACAICACTITGA 2340 2281 ACGCCCAGTIGAGICTCAAIACCTIGGAITIGCAACIGGAACAIGGAGACAICACITIGA 2340
TITICATIGICACCAACGAGGAGAGTICCATCCTGGCTGAACCTIGACAATCTCGAGTGA 126 CAAIAGTAAACACACCAGAIGTITICGAAATITIGACCACTIGCCTACCTITAGITCAC 132	ò 8	2341 AAGGATACAATTIGICCAAGICAGCCTIGCIGAGATCATITCIGAIGAACICACAGCAIG 2400 2341 AAGGATACAATTIGICCAAGICAGCCTIGCIGAGAICAITICIGAIGAACICACAGCAIG 2400
	Qy	2401 CTABABABABATCAAGCTATAATBACAGATGAAACAAATGACAGTTTGGTGGCTCCAC 2460 

6 B 6

KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 5597) AUTHORS Canfield, W.M. TITLE GloNAc phosphotransferase of the lysosomal targeting pathway JOURNAL Patent: US 6642038-A 4 04-NOV-2003; FEATURES 1.5597 Source /organism="unknown" /mol_type="genomic DNA"	Ouery Match Best Local Similarity 100.0%; Pred. No. 0; Matches 5597; Conservative 0; Mismatches 0; Indels 0; Gaps 0 Ov 1 CGGAGCCGAGCGGAGCGTCGTCGCCGGAGCTGCAATGAGCGGCGCGGAGGCTGGACC	CGGAGCCGAGCGGCGCTCGCCGCAGCTGCAATGAGCGGCGCCCGGAGGCTGTGACC 6	0y 121 GGCGGCTCCTCGGGGCGTGGCGTGGCGGTGAGGGTGATGCTGTTCAAGCTCC 180	QY         181 TGCAGAGACAAACCTATACCTGCCTGTGCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240           Db         181 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240	QY         241 GCGTCGTTGTCACCATCGTCTCCGCCTTCCGAGAGGTGGTTCTGGAATGGAGCC 300           Db         241 GCGTCGTTGTCACCATCGTCTCCGCCTTCCAGTTCGGAGAGGTGGTTCTGGAATGGAGCC 300	QY 301 GAGATCAATACCATGTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360	QY         361 AGAATGGGTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG         420           Db         361 AGAATGGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG         420	Qy         421 ATCTTGAACTACTGAAGGAACTACAGCAGGAGGACGAGAAGA         480	Qy         481         CAATGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAACCAGT         540           Db         481         CAATGAGAAATCCTTGGGAAAAACACACAGAACCTACTAAGAAGAGTGAGAAGCAGT         540	Qy         541 TAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCCCTGC         600           bb         541 TAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCCCTGC         600	Oy 601 CAGCCAACATCACCTGAAGGACGTGCCATCTCTTATCCTTTTTCATTCTGCCAGTG 660	Qy 661 ACATTITICAATGITGCAAAACCAAAAACCITGTACCAATGICICAGITGITGITTITG 720	OY 721 ACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAACAGAA 780	OY 781 CAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAG 840
Db   4621   CGTGCAGGTCTAATTTCAACAGGCTAGAGTTAGTACTTACCAGATGTAATTATGTTT   4680     Qy   4681   TGGAAATGTACATATTCAACAGAGTGCCTCATTTAGAAATGAGTAGTGCTGATGGCA   4740     Db   4681   TGGAAATTCAACAGAAGTGCCTCATTTTAGAAATGAGTAGTGCTGATGGCA   4740     Qy   4741   CTGGCACATTACAGTGGTGCTTTAATAACTCATTGGTAATTCCAGTAGCTATCTT   4800     Db   4741   CTGGCACATTACAGTGGTGCTTTATAATACTCATTGGTAATTCCAGTAGCTATCTT   4800     Qy   CTCAGTTACAGTGGTGCTTTAATACACTGAATACTCATTGTAAAAGGCTGGTATCTT   4800     Qy   CTCAGTTGGTTTTTGATAGAACAGAGGCCAGAACTTTCTTT	Qy         4861         AAATTATTGGGGCCACCTGTGTCTTTGTCATACATTCTTCTTGCTGTTGTTTAGTTTGT         4920           bb         4861         AAATTATTGCAGCCACCTGTGTCTTTGTCATACATTCTTGTTGTTGTTTAGTTTGTTGT         4920           Qy         4921         TTTTTTTCAAACAACCTCTAAAAAACAAACCATGTTTAGCTTGCACTGTACAAAA         4980	4921 TITITICAACAACCICTAAAATGIAAAAACCATGITTAGCITGCAGCIGIACAAA 498 4981 ACTGCCCACCAGCAGATGTAGACCTCAGGCCATTACCAATCACTGCAATTATTT 504 4981 ACTGCCCACCAGCAGATGTGACCCTCAGGCCATCACTTGCCAATCACTGAGAATTATTT 504 4981 ACTGCCCACCAGCAGATGTGACCCTCAGGCCATCACTTGCCAATCACTGAGAATTATTT 504	QY         5041         TIGITGITGITGITGITGITTITGAGACAGAGICTCTCTCTGTGCCCAGGCTGGAG         5100           bb         5041         TIGITGITGITGITGITGITGITGITGITGAGACAGAGTCTCTCTCTCTGTTGCCCAGGCTGGAG         5100	Oy 5101 IGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCGGCTTCAAGCAGTTCTGTC 5160	OY 5161 TCAGCCTTCTGAGTAGCTGGGACTACAGGTGCATGCCACCACACCTGCTAATTTTTGTA 5220  bb 5161 TCAGCCTTCTGAGTAGCTGGGACTACAGGTGCATGCCACCACCACCTGCTAATTTTTGTA 5220	QY         5221         TITITAGIAGACGGGGTTCCACCATATTGGTCAGGCTTATCTTGAACTCCTGACCTC         5280           bb         5221         TITITAGTAGAGGGGTTCCACCATATTGGTCAGGCTTATCTTGAACTCCTGACCTC         5280	OY 5281 AGGIGATCCACCTGCCTCCCCAAAGTGCTGAGATTACAGGCATAAGCCAGTGCAC 5340  bb 5281 AGGIGATCCACCTGCCTCCCCAAAGTGCTGAGATTACAGGCATAAGCCAGTGCAC 5340	QY 5341 CCAGCCGAGAAITAGTAITTTTAGGAGTTAAACCTTGGCGTCTAGCCATATTTATG 5400  5341 CCAGCCGAGAAITAGTAITTTTATGTATGATAAACCTTGGCGTCTAGCCATAITTTATG 5400	QY 5401 TCATAATACAATGGATTTGTGAAGAGAGATTCCATGAGTAACTCTGACAGGTATTTTAG 5460  bb 5401 TCATAATACAATGGATTTGTGAAGAGCAGATTCCATGAGTAACTCTGACAGGTATTTAG 5460	OY 5461 ATCATGATCTCAACAATATTCCTCCCAAATGGCATACATCTTTTGTACAAGAACTTGAA 5520  bb 5461 ATCATGATCTCAACAATATTCCTCCCCAAATGGCATACATCTTTTGTACAAAGAACTTGAA 5520	OY 5521 ATGTAAATACTGTGTTTGTGCTGTAAGAGTTGTGTATTTCAAAAACTGAAATCTCATAAA 5580  Db 5521 ATGTAAATACTGTGTTTGTGCTGTAAGAGTTGTGTATTTCAAAAACTGAAATCTCATAAA 5580	Oy 5581 AACTTAAATTTTGAAA 5597 		DEFINITION Sequence 4 from patent US 6642038.  ACCESSION AR428739.1 GI:40188473

TTGGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTCATAATGCACAGTGGAA TTCGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTCATAATGCACAGTGGAA TTCGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTCATAATGCACAGTGGAA TGAATGCCACCACAATACATTTAATCTCACGTTTCAAAATACAAACGATGAAGAGTTCA TGAATGCCACCACAATACATTTTAATCTCACGTTTCAAAATACAAAACGATGAAGAGTTCA AAATGCCACCACAATACAAT	216 222 222 222		2341 AAGGATACAATTIGTCCAAGTCAGCCTTGCTGAGATCATTTCTGATGAACTCACAGCATG 2400	2461 AGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGATTGC 2520 2461 AGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAAATTGC 2520 2521 AGGGTTGACTTTTCCTGCAGTGAGTGTAAAAGTGAATGGTATGACCATGACCAGGTCAGAATGC 2580	CACCCCTGGACTTGGAGACCACGCAGATTTAGGGTGGAAACTCACCCCAAAAACCACCCAAAAACCACCCGAAAAACCACCCGAAAAACCACC	2641 TAGGGGAAATGTGACAAAAGAAAGCCCCATCTCTGATTGTTCCACTGGAAAGCCAGG 2700 2701 TGACAAAAGAAAAGAAAATCACGGGAAAGAAAAAAAAGAAAACAGTAGAATGGAGGAAAATG 2760 2701 TGACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		2881 AAGAAGACTCATTGAAGACACAATTGGCATACTTGACTGATAGCAAAATACTGGGAGGC 2940 2881 AAGAGACTCATTGAAGACACAATTGGCATACTTGATGGCAAAAATACTGGGAGGC 2940 2941 AACTAAAAGATACATTGGCAATTGCCAGATATTGAAATAAAT
8 8 8 8 8	\$\frac{1}{2}\$	, de	\text{\text{O}} \text{\text{O}} \text{\text{O}} \text{\text{O}} \text{\text{O}}	\$ 40 \$ 60	\$ g \$	4 6 6	4 6 4	8 8 8 8
	1021 AGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATT	ACGAGGACTICGGGGTTCGGGGGGGGGGGGGGGGGGGGGG	CAATAGTAACACCAGGATGTTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGTTCAC [	1321 CTGCTATTGAAAGTCACATTCATCGAAGGGCTGTCCCAGAAGTTTATCCTAA 1380 1381 ATGATGATGTTTGGGAAGGATGTCTGGCCAGATGATTTTACAGTCACTCCAAAG 1440 1381 ATGATGATGTTTGGGAAGGATGTCTGGCCAGATGATTTTACAGTCACTCCAAAG 1440 1381 ATGATGATGTTTGGGAAGGATGTTTGGCCAGATTTTTACAGTCACTCCAAAG 1440 1441 GCCAGAAGGTTTATTGACATGCCTGGCCAAACTGTGCGAGGCTGCCAGGTTCCT 1500	1441 GCCAGAAGGTTTATTTGACATGGCCTGTGCCAACTGTGCCGAGGGCTGCCCAGGTTCCT 1500 1501 GGATTAAGGATGGCTATTGTGACAAGGCTTGTAATAATTCAGCCTGCGATTGGATTGGTG 1560 1501 GGATTAAGGATGGCTATTGTGACAAGGCTTGTAATAATTCAGCCTGCGATTGGGATGGTG 1560 1561 GGGATTGCTCTGGAAACAGTGGAAGGCTTGTAATATTGCAGGAGGTGGAATGGTA 1560		1681 ATCAGGGATGTGCGATTCCTGGCTCGCTGATAAGTTCTGTGACCAAGCATGTCT 1740	TGATCCTTCTCCCAAACCAGACTCACTATATTATTCCAAAAGGTGAATGCCTGCC

301 GAGATCAATACCATGTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360 301 GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360 361 AGAATCGGCTTTGTTTGTTTGATTGAGACAATATTGGGAAAAGTCCTTTC 360 361 AGAATCGGCTTTGTTCTGCCCATGACGATTGATGTTTTTACACTGGGTGAATGGCAAAG 420 361 AGAATCGGGTTTGTTTGTTTGTTTTTTTTTTTTTTTTTT	21 ATCTTGAACTACTGAAGGAACTACAGCTCAGAACAGAAC	481 CAATGAGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAGCAGT 540 	541 TAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCCCTGC 600	601 CAGCCAACATCACCCTGAAGGACGTGCCATCTTTTATCCTTCTTTTCATTCTGCCAGTG 660 [	661 ACATTITCAAUGITGCAAAACCAAAAACCCTTCTACCAAIGICTCAGITGITITIG 720 	721 ACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGACAGA	781 CAGIATGGAGGGGGTACTTGACAACACATAAAGAAGTCCCTGGATTAGTGCTAATGCAAG 840 	841 ATTIGGCTTICCTGAGIGGATITCCACCAACATTCAAGGAAACAAATCAACTAAAAAAAA 900 	901 AAITGCCAGAAAAICTITCCTCTAAAGICAAACIGTIGCAGITGTATICAGAGGCCAGIG 960 	961 TAGCGCTTCTAAAACTGAATAACCCCAAGGATTTTCAAGAATTGAATAAGCAAACTAAGA 1020 	1021 AGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATT	1081 TGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTGAAGATA 1140 	1141 ACGAAGAACTGAGTACTCATTGCGATCTATCGAGGCATGCACCATGGGTTCGGAATA 1200	1201 TTTTCATTGTCACCAACGGGCAGATTCCATCCTGGCTGAACCTTGACAATCCTCGAGTGA 1260 	1261 CAATAGPAACACACAGGATGTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGTTCAC 1320 	1321 CTGCTATTGAAAGTCACATTCATCGCATCGAAGGGCTGTCCCAGAAGTTTATTTA	
6 6 6	% ଶ	S do	Q do	VQ.	QY Db	yo, du	QY Db	QY Db	, dg	OY DP	oy B	\$ g	S a	oy Db	9 Q	65 da	
QY         5221 TTTTTAGTAGAGGGGTTCCACCATATTGGTCAGGCTTATCTTGAACTCCTGACCTC         5280           Db         5221 TTTTAGTAGAGGGGTTCCACCATATTGGTCAGGCTTATCTTGAACTCCTGACCTC         5280           CO         5281 AGTGATCCACCTGCCTCTGCCTCCCCAAGGGCTTATCTTGAACTCCTGACCTC         5280           CO         5281 AGGGATCACCTGCCTCCCAAAGTGCTGAGATTACAGGCATAAGCCAGTGCAC         5340           Db         5281 AGGTGATCCACCTCCCCAAAGTGCTGAGATTACAGGCAATGACCAGTGCAC         5340	TTTATG 5	QY 5401 TCATAATACAATGGATTTGTGAAGAGCAGATTCCATGAGTAACTCTGACAGGTATTTTAG 5460	Qy 5461 ATCATGATCTCAACAATATTCCTCCCAAATGGCATACATCTTTTGTACAAAGAACTTGAA 5520	QY 5521 ATGTAAATACTGTGTTTGTGCTGTAAGAGTTGTGTATTTCAAAAACTGAAATCTGTAAAA 5580 	Qy 5581 AAGTIAAATTTGAAAA 5597 	I 3 828	DEFINITION Sequence 4 from patent US 6670165. ACCESSION AR442828 VERSION AR442828.1 GI:42670304	SOUNCE Unknown. ORGANISM Unknown. Unlassified.	AUTHORS Cantield, W.M. AUTHORS Cantield, W.M. TITLE Methods for producing highly phosphorylated lysosomal hydrolases JOHNAL Patent: US 667016-7, 4 30-DEC-2003;	r C	y Match 100.0%; Score 5597; DB 6; Length 5597; Local Similarity 100.0%; Fred. No. 0; have Eed. Action 100.0%; Minmails of Constitution 100.0%; Minmails of Constituti	CGGAGCCGAGCGGCGTCCGTCGCGAGCTGCAATGAGCGGCGCCCCGGAGGCTGTGACC 60	61. IGCGCGCGGCCCCACCCCGAATGCGGCTCGCTGAAGGCGCGCGGCGGCGCGCTCCTAATGCGCGGCTCGCTGAAGCGGCGGCGGCGGCGGCTCCTAATGCGCGGCTCGCTGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	121 GGCGCTCACGGGGCCCCTGAATGGCGGCTCGCTGAGGCGGCGGCGGCGGCGGCGGCGGCCGGC	181 IGCAGAGACAAACCTATACCTGCCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG	DD 181 TGCAGAGACAAACCTATACCTGCCTGCCTGCCTGGGGTATGGGCTCTACGTGTGCTTCTTGG 240 QY 241 GCGTTGTCACCATCGTCTCCGCCTTCCAGTTCGGAAGGTGGTTCTGGAATGAGCC 300 DD 241 GCGTCGTTGTCACCATCGTCTCCCGCCTTCCAGTTCGGAAGGTGGTTCTGGAATGAGCC 300	

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AB033034.2 GI:20521791	4621 CGTGCAGGTCTAATTTCAACAGGCTAGAGTTAGTACTACTTACCAGATGTAATTATGTTT 4680   -  -	Qy Db
AB033034 LOCUS AB033034 DEFINITION Homo sapiens mRNA for KIAA1206	4561 ATTGACATCTGAAATGCTTTGTAATTATTGACTTCAGCCCCTAAGAATGCTATCAATTCA 4620	ž d
	TTTTATTATTATTTAGACTGTAAATGGTCTTAAACCACTAACTA	qa
OY 5581 AAGTIAAATTTTGAAAA 5597 	TITITATIAATATITAAGACIGTAAATGGICTITAAACCACTAACTGAAGAGCICAATG 4	λO
	4441 TAGAIGTIATITAAATAAGCAGCAATATCACCTCTTATTGACAATACCTAAATTATGAG 4500 	Qy Db
Db 5461 ATCATGATCTCAACAATATTCCTCCCAA	4381 AGITAACTAGTTATTCTTGGGTATAGGGATTGGGGTGTCTAAACCTATTTTA 4440	ZZ GG
Qy 5461 ATCATGATCTCAACAATATTCCTCCAA	4321 AGCCTTTTGCTAAAGTTTTGCACTTTTTTTTTTTTCATTTTCCCATTTTTTAAGTAGTTACTA 4380	a :
Db 5401 TCATAATACAATGGATTTGTGAAGAGG	AGCCTTTTGCTAAAGTTTTGGACTTTTTTTTTTTTTAGACTTTTTAAGTAGTTACTA	0y
5341	4261 TAGGAGAAGCCTATGCCAGCTGGGAGTGATTGCTAAGAGGCTCCAGTCTTTGCATTCCAA 4320	හි අධ
Db 5281 AGGTGATCCACCTGCCTCTGCCTCCCCTCCCACCTCCCACCTCCCACCTCCACCTCCACCTCCACCA	4201 GGCTCACTGACAGAGACAGCTGTTAATTTCCCACAGCAATCATTGCAGACTAACTTTAT 4260	6 G
Qy 5281 AGGTGATCCACCTGCTCTGCCTCCCCA	TCTGAACTGATTTTACTTTTAAAGAATTTGCTCATGGACCTGTCTTTTTTTT	qa
	TCTGAACTGATTTTACTTTTAAAGAATTTGCTCATGGACCTGTCATCCTTTTTAAAAA	ò
	4081 TATAGCCCACTGACTAGGAATTATTTAACCAACTGAAAACTTGTGTGTG	λο i
Db 5101 TGCAGTGCGCAATCTCAGCTCATTGTTTTTTTTTTTTTT	4021 GCTTAGCAGTTTGGCCCGAAGAAAAATATCCAGTACCATGCTGTTTTGTGGCATGA 4080	<b>7</b> 20
5101	ccrcaccattractgaggartrtaaaacrcaggrtcacagargrctrtgrgargrgar	qu
Oy 5041 INGTIGITIGITIGITIGITIGITITITIGI 	CCTCAGCATTTACT	λΌ
Db 4981 ACTGCCCACCAGCCAGATGTGACCCTC	3901 ACAAAGAAGCTAGTCCCAATCGAATCAGAGTATAGAAGATCTTCATTTGAAAACCATCTA 3960 	Qy Db
4921	3841 CATTTTTGCTGAGCAGTTAATTGCACTTAAGCGGAAGATATTTCCCAGAAGGAGATAC 3900 	& 43 6
4861	3781 ACAARITGAAGTITIGGACCCATIGIGIACIAGCAACAITGAITAIGITIACIAITAIT 3840 	oy Qb
Db 4801 CTCAGTTTGGTTTTTGATAGAACAGAGGGGGGGGGGGGG	3721 GAGAGTATCGAAACCGTTTCCTTCATATGCATGAGGCTGCAGGAATGGAGGGCTTATCCAG 3780 	oy Oy
Oy 4801 CTCAGTTGTTTTGATAGAACAGAGGG	CIGITETECAGGGACTICTATGAATCCATGTICCCCATACCTTCCCAATTIGAACTGCCAA 372	qa
	CTTTCTCAGGGGTTCTATGAATCCATGTTCCCCATACCTTCCCAATTTGAACTGCCAA	? <i>*</i> 6
Db 4681 TGGAAATGTACATATTCAAACAGAAGT	3601 AGTITGTITGCCTGAATGACAACAITGACCACAAICATAAAGAIGCTCAGACAGTGAAGG 3660 3601 AGTITGTITGCTTGAATGACAAACAAAAAAAAAAAAAAAA	ે દે
	3541 TTCGTACCAACGTTCTCATGTGGTTGGCCAGTTGGATGACATAGAAAAACCCTAGGA 3600	qa

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PRI 10-MAY-2002 CAGGCCATCATTGCCAATCACTGAGAATTATTT GAGA CAGAGITCITCITCITGITGCCCAGGCIGGAG CAACCTCCGCCTCCCGGGTTCAAGCAGTTCTGTC AGGIGCATGCCACCACCTGCTAATTTTGTA ATATTGGTCAGGCTTATCTTGAACTCCTGACCTC TGTCATACATTCTTCTTGCTGTTGTTTAGTTTGT bp mRNA linear 08 protein, partial cds.

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GAATGCCACCACAATACATTTTAATCTCACGTTTCAAAATACAAACGATGAAGAGTTCAA
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                                                                                                                                                            181 AATAGTAACACCAGGATGTTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGTTCACC
                                                                                                                                                                                                                                                                                          1862 CAGCTTTGCAGAAGTAGCCAAAAGAGGAGTTGAAGGTGCCTATAGTGACAATCCAATAAT
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                                                                                                                                                                                                                                                     1382 TGATGATGTCATGTTTGGGAAGGATGTCTGGCCAGATGATTTTTACAGTCACTCCAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 TGATGATGTCATGTTTGGGAAGGATGTCTGGCCAGATGATTTTTACAGTCACTCCAAAGG
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                                                                                                                                                                                                                                  prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
DNA Res. 6 (5), 337-345 (1999)
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/ Droduis = "KIAA1208 protein"
/ Droduis = "KIAA1208 protein"
/ Drodein id="BA86522.2"
/ Drotein id="BA86522.2"
/ Lanslation="A1150520Proper Search From Protein id="BA86528.2"
/ translation="A11505X0Proper Search From Protein Interpretation="A11505X0Proper Search From Protein Interpretation="A11505X0Protein Interpreta
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REVETHPTAKEKTGKEKERBNRENEDALENTGA
TEVLLGREKLGHYTDSQYTIGGNVTREEPPALSEKERSKERBNRENEDALENTIGA
TEVLLGREKLGHYTDSYLGFLEWEKKYFQDLLDBESSLKTQLAYFTDSKNTGRQLKD
FADSLRYVNKILLNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS
EMDGFAKFSTYLMSAVQFALISQVPBUVTDQSGYLSDREIBTALLAFHELFLSLQD
LTGLEEHMLINGSKMLFADITQLANIPPTGESYDBNLPPPVTKSLVYNCKPVTDKIHKA
YKDKNKYRFELMGEBEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obara,O., Nagase,T. and Kikuno,R.

Ohara,O., Nagase,T. and Kikuno,R.

Direct Submission

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MFTIPSFFAEQLIALKRKIFPRRRIHKEASPNRIRV"
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/clone lib="pBluescriptII SK plus"
/note="This sequence was replaced that of fg05318 cDNA as
a representative CDNA sequence for KIAA1208."
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                                        Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                      Nagase, T., Ishikawa, K., Kikuno, R., Hirosawa, M., Nomura, N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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/note="Start codon is not identified."
/codon_start=2</pre>
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fj07955"
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Matches 4502; Conservative 0
           sapiens (human)
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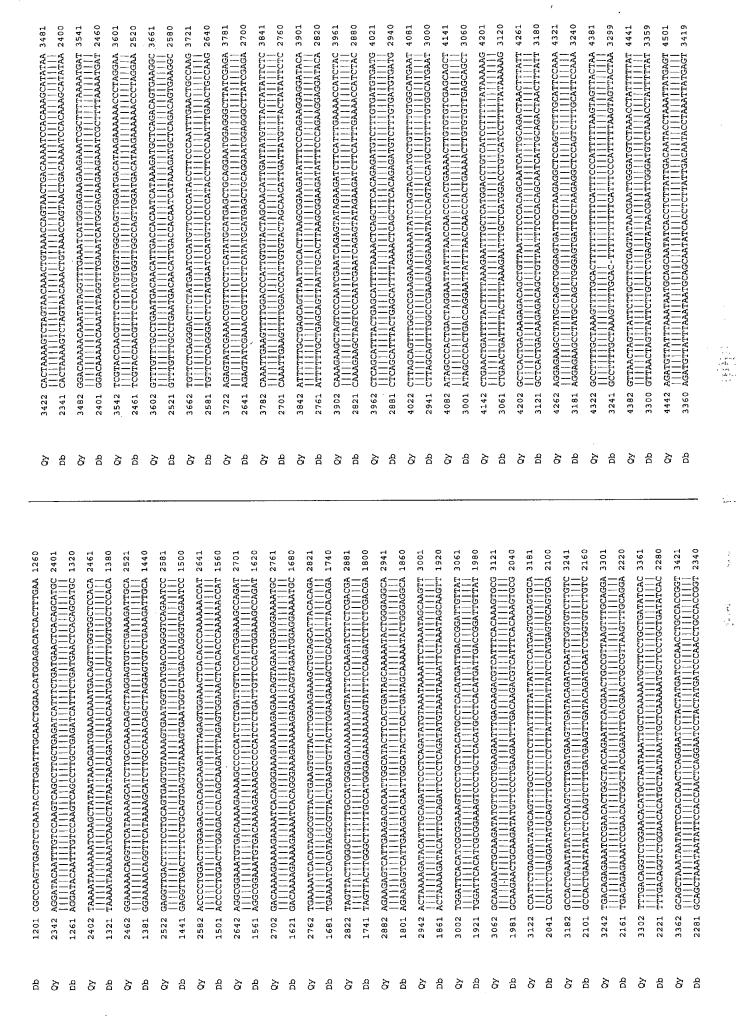
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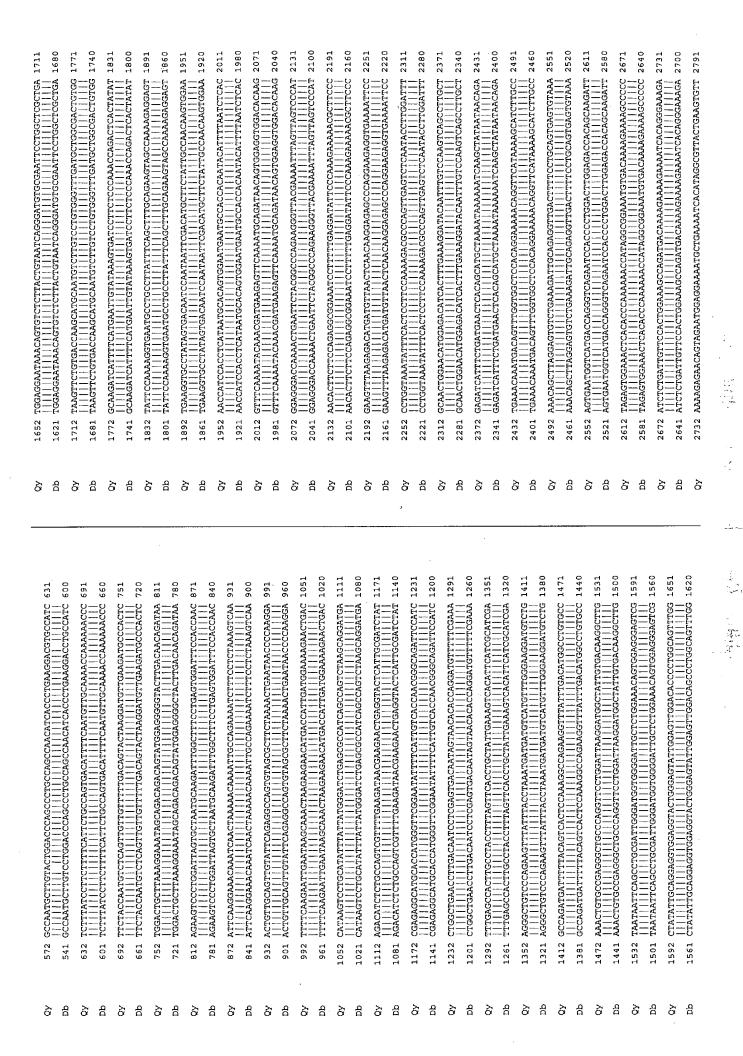
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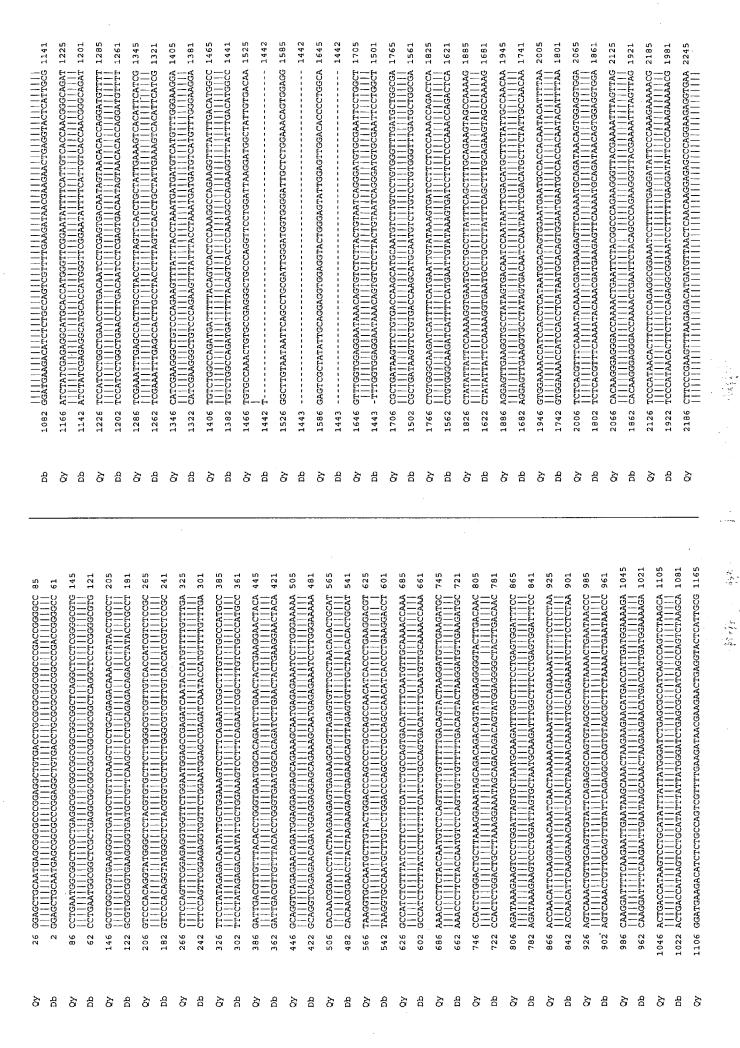
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Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
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Nucleic acid-associated proteins
Nucleic acid-associated proteins
Incyte Genomics, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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|db xref="taxon:5606"
|noTe="Incyte ID No: 2749402CB1"
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99.7%; Pred. No. 0;
iive 0; Mismatches
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Sequence 25 from Patent W00250279.
AX468102 AX468102.1 GI:21900976
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Best Local Similarity 99.7
Matches 4354; Conservative
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Db 3781 AGCAACATTGTTTACTATATTTTTCCATTTTTTTCCAACCAA	RESULT 6 Ax468106 LOCUS LOCUS LOCUS Sequence 29 from Patent W00250279. AX468106 VERSION KEYWORDS SOURCE Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE Baughin, M.R., Lu, Y., Arvizu, C., Ramkumar, J., Yao, M.G., Policky, J.L., Walia, N.K., Tirboulay, K.M., Yue, H., Batra, S., Ding, L., Lal, P.G., Borowsky, M.L., Lu, D.A., Gandhi, A.R., Ding, L., Lal, P.G., Borowsky, M.L., Lu, D.A., Gandhi, A.R., Cariffin, J.A., Xu, Y., Azimzai, Y., Gietzen, K.J., Tang, Y.T., Marren, B.A., Mason, P.M., Bufford, N., Hafalia, A.J., Lee, S.Y., Yang, J., Gorvad, A.E., Emerling, B.M., Marquis, J.P., Lee, S.Y., Yang, J., Gorvad, A.E., Emerling, B.M., Marquis, J.P., Lee, S.Y., Yang, J., Gorvad, A.E., Emerling, B.M., Marquis, J.P., Lee, S.Y., TITLE Nucleic acid-associated proteins JOURNAL Patent: WO 0250279-A 29 27-UUN-2002; Incyte Genomics, Inc. (US) FEATURES  1. 4277 And J.YDe="Homos sapiens" And Lype="Homos sapien
	3332 TTGCTCAAAATGCTTCCTGCTGATATCACGCAGCTAAATATTTCCACCCAC



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Canfield, W.M.

GalCNAc phosphotransferase of the lysosomal targeting Patent: Location/Qualifiers Score 3761; DB 6; Length 3 Pred. No. 0; 0; Mismatches 10; Indels /organism="unknown" /wol\_type="genomic DNA Query Match
Best Local Similarity 99.7%;
Matches 3767; Conservative 1. .3783 KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES ORIGIN g ò 8 8 2 4 5 6 5 6

CCTACCTTTAGTTCACCTGCTATTGAAAGTCACATTCATCGCATCGAAGGGCTGTCCCCAG GACAATCCTCGAGTGACAATAGTAACACCCAGGATGTTTTTCGAAATTTGAGCCACTTG TACAGTCACTCCAAAGGCCAGAAGGTTTATTGACATGGCCTGTGCCAACTGTGCCGAAGTTGCGAGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAG CATGAATTGTATAAAGTGATCCTTCTCCCAAACCAGACTCACTATATTATTCCAAAAGGT GAATGCCTGCCTTATTTCAGCTTTGCAGAAGTAGCCAAAAGAAGAGGTGCCTAT AGTGACAATCCAATAATTCGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTC GAATGCCTGCCTTATTTCAGCTTTGCAGAAGTAGCCCAAAAGAGGAGTTGAAGGTGCCTAT AGTGACAATCCAATAATTCGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTC CATGAATTGTATAAAGTGATCCTTCTCCCAAACCAGACTCACTATATTATTCCAAAAGGT 

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Sy qa	3045 ATTGACCGGATTGTTATGCAAGAACTGCAAGATATGCTCCCTGAAGAATTTGACAAGACG 3104 	AUTHORS Cantletd, W.W. TITLE Methods of treating lysosomal storage diseases JOURNAL Patent: 0.8 6537785-A 21 25-MAR-2003; FEATURES Location/Qualifiers
oy OD	3105 TCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTTATTTTTATTAT 3164 2947 TCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTCTTTTTATTATTAT 3006	SOUICE 1.35041 /organism="unknown" /mol_type="genomic DNA"
Db Qy	3165 CTCATGAGTGCAGCGACTGAATATATCTCAAGTCTTTGATGAAGTTGATAAAA 3224 	Query Match Best Local Similarity 99.7%; Pred. No. 0; Matches 3492; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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2037 TTCAAAATGCAGATAACAGTGGAGGTGGACACAAGGGAGCGACCAAAACTGAATTCTACG 2096	7 GCCCAGAAGGGTTACGAAATTTAGTTAGTCCCATAACACTTCTTCCAGAGGGGGAAATC 215	2157 CTITITGAGGATATTCCCAAAGAAAACGCTTCCCGAAGTTTAAGAGACATGATGTTAAC 2216	2217 TCAACAAGAAGCCCAGGAAGAGGTGAAAATTCCCCTGGTAAATATTCACTCCTTCCA 2276 2035 TCAACAAGGAGCCCAGGAAGGTGAAAATTCCCCTGGTAAATATTTCACTCCTTCCA 2094	2277 AAAGACGCCCGGTTGAGTCTCAATACCTTGGATTTGCAACTGGAACATGGAGACATCACT 2336 2095 AAAGACGCCCGGTTGAGTCTCAATACCTTGGATTTGCAACTGGAACATGGAGACATCACT 2154	TTGAAAGGATACAATTTGTCCAAGTCAGCCTTGCTGAGATCATTCTGATGAACTCACAG 23 	CATGCTAAAITAAAAATCAGCTATAATAACAGATGAACAAATGACAGTTTGGTGGCT 245 	CCACAGGAAAACAGGITCATAAAAGCATCTIGCCAAACAGCITAGGAGTGITCIGAAAGA 2 	TIGCAGAGGTIGACTITICCTGCAGTGAGTGTAAAATGAATGGATGGTCATGACCAGGGTCAG	2577 AATCCACCCTGGACTTGGAGACCACGCAGATTTAGAGTGGAAACTCACACCCAAAAA 2636 	ACCATAGGGGGAAATGTGACAAAAGAAAGCCCCCATCTCTGATTGTTCCACTGGAAAGC 269	2697 CAGATGACAAAAGAAAATCACAGGGAAAGAAAAGAAAGAA	2757 AATGCTGAAAATCACATAGGGGTTACTGAAGTGTTACTTGGAAGAAAGCTGCAGCATTAC 2816 2575 AATGCTGAAAATCACATAGGGGTTACTGAAGTGTTACTTGGAAGAAAGA	ACAGATAGTTACTTGGGCTTTTTGCCATGGGAGAAAAAAAA	7 GACGAAGAAGACCATTGAAGACACAATTGGCATACTTCACTGATAGCAAAATACTGGG 293 	7 AGGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGTAAATAAA	2997 AAGTTIGGATTCACATGGGGAAAGTCCCTGCTCACATGCCTCACATGATTGACGGGATT 3056 [11	7 GTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGACAAGACGTCATTTCACAAA 3	317
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Qy 3177 GIGGAGCCACTGAATATCTCAAGTCTTTGATGAAGTTGATACAGATCAATCTGGTGTC 3236	ζς qq	357 TITCAGAAICGGCTITGICTGCCCAIGCCGAITGACGITGITTACACCTGGGTGAAIGGC 416
Qy 3237 TIGICIGACAGAGAAATCCGAACACTGGCTACCAGAATTCACGAACTGCCGTTAAGTTTG 3296  Db 3055 TIGICIGACAGAGAAATCCGAACACTGGCTACCAGAATTCACGAACTGCCGTTAAGTTTG 3114	<i>&amp;</i> 43	417 ACAGATCTTGAACTACTGAAGGAACTACAGCAGGTCAGAQAACAGATGGAGGAGGAGGAG 476
Qy 3297 CAGGATTTGACAGGTCTGGAACACATGCTAATAAATTGCTCAAAAATGCTTCCTGCTGAT 3356	& 6	477 AAAGCAATGAGAAAATCCTTGGGAAAACACAACGGAACCTACTAAGAAGGGGGGGG
Qy 3357 ATCACGCAGCTAAATAATATTCCACCAACTCAGAATCCTACTATGATCCCAACTGCCA 3416	<i></i>	537 CAGTTAGAGTGTTTGCTAACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCC 596
Qy 3417 CCGGTCACTAAAAGTCTAGTAACAAACTGTAAACCAGTAACTGACAAAATCCACAAAAGGA 3476  Db 3235 CCGGTCACTAAAAGTCTAGTAACAAACTGTAAACCAGTAACTGACAAATCCACAAAAGGA 3294	<i>≿</i> 8	597 CTGCCAGCCAACATCACCCTGAAGGACGTGCCATCTTTATCCTTTTATATTTTTTTT
Qy 3477 TATAAGGACAAAAACAAATATAGGTTTGAAATCATGGGAGAAGAAATCGCTTTTAAA 3536 	<i></i> у 40	657 AGTGACAITHICAAHGIIGCAAAACCAAAAAACCCTICTACCAATGTCTCAGIIGITGII 716 
QY 3537 ATGAITCGTACCAACGTITCTCAUGTGGCCAGTTGGATGACATAAGAAAACCCT 3596 	λ O	717 ITIGACAGIACTAAGGAIGITGAAGAIGCCCACTCTGGACTGCTTAAAGGAAAIAGCAGA 776
Oy 3597 AGGAAGTTTGTTTGCCTGAATGACAACATTGACCACAATCATAAAGATGCTCAGACAGTG 3656  1415 AGGAAGTTTGTTTGCCTGAATGACAACATTGACACAATCATAAAGATGCTCAGACAGTG 3474	& 43	777 CAGACAGTATGCAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAAIG 836
Qy 3657 AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCATACCTTCCCAATTTGAACTG 3716	<i>&amp;</i> 8	837 CAAGATTIGGCITICCIGAGIGGATITCCACCAACATICAAGGAAACAAAICAACIAAAA 896 
OY 3717 CCAAGAGATATCGAAACCGTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGCTTAT 3776	ò 8	897 ACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC 956
Oy 3777 CGAGACAAATTGAAGTTTTGGAC 3799  Db 3595 CGAGACAAATTGAAGTAGTG 3617	& a	957 AGTGTAGGGCTTCTAAAACTGAATAACCCCAAGGATTTTCAAGAATTGAATAAGCAAACT 1016 
	දු පු	1017 AAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATT
LCCUS AR442838 3621 bp DNA linear PAT 20-FEB-2004 DEFINITION Sequence 21 from patent US 6670165. ACCESSION AR42838 VERSION AR442838.1 GI:42670314	oy Oy	1077 GATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTGCGCAGTCGTTTTGAA 1136
_	රු සි	1137 GATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAAGGCATGCAT
REFERENCE 1 (bases 1 to 3621) AUTHORS Canfield, W.M. AUTHORS Methods for producing highly phosphorylated lysosomal hydrolases JOURNAL Patent: US 6670165-A 21 30-DEC-2003;	à a	1197 AATATTTTCATTGTCACCAAGGGGGAGATTCCATCCTGGCTGAACCTTGACAATCCTCGA 1256 1015 AATATTTTCATTGTCACCAAGGGGGGAGATTCCATCCTGGGTGAACCTTGACAATCTTCGA 1074
ø	λό G	1257 GIGACAATAGTAACACACCAGGAIGTTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGT 1316
ore 3485.4; DB 6; Length 3621;	Sy Dp	1317 TCACCTGCTATTGAAAGTCACATTCATCGCATCGAAGGGCTGTCCCAGAAGTTTATTTA
; conservative AGCCGAGATCAATACCATG	ò	1377 CIAAATGATGATGATGTTTGGGAAGGATGCTGGCCAGATGATTTTTACAGTCACTCC 1436

1315 TTTCCAGAGCTTCACTTTCCTCCAGTGATTAAACTCAATGGTCATCACCAGGGTCAG 239 1316 TTCCAGAGCTTCACTTTCCTCCAGTGATTAAACTCAATGGTCAATCACCCAGGAAA 245 1317 ATTCCACCCCTGCAACTTTCCATCACCAGAATTTAAACTCAATCACCCCAAAA 245 1318 ACCATCACACCTCCAAAACAAAACAAAACAAAACAAAA	3537 ATGATTCGTACCAACGTTTCTCATGGTTGGCCAGTTGGATGACATAAAAAACCCT 3596
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1135   CTANANTARIANTARIANTARIANTARIANGANACTUCCOCCACATUCCOCCANACTUCCOCCANACTUCCOCCACATUCCOCCANACTUCCOCCACATUCCOCCANACTUCCOCCACATUCCOCCANACTUCCOCCACATUCCOCCACATUCCOCCACATUCCOCCANACTUCCOCCACA	Qy         2457         CCACAGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGA         2516           Db         2275         CCACAGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAAA         2334

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LKDTPADLSTAYVNKILNSKGFTSKYVRAHVPHINDIRDINGBLQDMPPBEPBKYSFHK
VRASDWÇFAPSYFYXLMSAVQPLAISQVPDBVDTQOSGVLSDREIRTLATRIHELPL
SLQDLFGEHMLINGSKMLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDK
KHAYKDKWYKRFEINGEBIAFKMITTNVSHYVQQLDDIRANPRKFYCLNDNIDHNH
KDAQTYKAVLADFYSSMFPIPSQFELPREYNRRFLHHHELQBWRAYRDKLHTRY
ATLIMFTIFSFFAEQLIALKRKIFPRRIHKEASPNRIRV
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                                               3474
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ETTARFRVETHTQKTIGGNVTKEKPPSLIVPLESQMTKEKKITGKEKENSRMEENAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3150)
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Submitted (02-DN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 52 Row: c Column: 9.
Location/Qualifiers
                                                                                                                      AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCATACCTTCCCCAATTTGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center General Conter code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contect: amg@bcm.tmc.edu
Gunatarie, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Xowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                          CCAAGAGAGTATCGAAAACCGTTTCCTTCATATGCATGAGCTGCAGGAATGGACTTAT
                                               AGGAAGTTTGTTTGCCTGAATGACAATGACCACAATCATAAAGATGCTCAGACAGTG
                                                                                             AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCATACCTTCCCAATTTGAACTG
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Homo sapiens, Similar to v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian), clone IMAGE:4470615, mRNA,
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4470615"
/tissue_type="Liver, adenocarcinoma"
/clone_lib="NHH MGC_90"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATC
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/note="Vector: pCMV-SPORT6"
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Hiraoka,S., Saga,Y., Seino,S., Nishimura,M., Kaisho,T., Hoshino,K.,
Kitamura,H., Nagase,T., Ohara,O. and Koga,H.
Kitamura,H., Nagase,T., Ohara,O. and Koga,H.
Prediction of the Coding Sequences of Mouse
KIAA-Monlogous cDNAs Identified Sequences of 500 Mouse
KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences
of CDNA Clones Randomly Sampled from Size-Fractionated Libraries
INS (bases 1 to 5204)
Cocazaki,N., Kikuno,R.F., Nagase,T., Ohara,O. and Koga,H.
Direct Submission
Submitted (19-MAY-2004) Hisashi Koga, Kazusa DNA Research
Institute, Laboratory for Genome Informatics, 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(B-mail:mouse@kazusa.or.jp, Tel:81-438-52-3919, Fax:81-438-52-3918)
The CREATE program supported by Japan science and technology
corporation; CDNA ilbrary construction, clone selection and 5'- &
3'-end one pass sequencing:
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QGCANSWLADKFCDQACNVLSCGFDAGDCGQDHFHELYKVTLLPNGTHTVVPKGEYLS
YEFRANIARRGVEGTYSDNPIIRHAG IANKWRTHILIMAGMNATTIYFNLTLGNAND
EEFKIQIAVEVDTEAFKLMSTTQKAYESIVGFVTPLPQADVPFEDVPKEKRFPKIRK
HDVNATGRFQEEVKIPPVNISLLPKEAQVRLSNLDLQLERGDITLKGYNLSKSALLRS
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KGFQELNKQTKKNMTIDGKELTISPAVLLWDLSAISOSKQDEDVSASRPEDNEELRYS
LRSIERHAPWVRNIFIVTNGQIPSWLNLDNPRVTIVTHQDIFONLSHLPTFSSPAIES
3061 AAATGTAAATACTGTGTTTGTGCTGTAAGAGTTGTGTATTTCAAAAACTGAAATCTCATA 3120
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/product=mKIAA1208 protein"
/protein_id="BAD32410.1"
/db_xref="G1:50510849"
/fb_xref="G1:50510849"
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EWSRDQYHVLFDSYRENIAGKSFQNRLCLPMFIDVVTWVNGTDLELLKELQQVREHM
EBSRDQYHVLFDSYRENIAGKSFQNRLCLPMFIDVVTWVNGTDLELLKELQQVREHM
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RDHALNPPPVLETWARLAQPTLGVTVSKENLSPLI VPPESHLPKEEESDRAEGNAVPV
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1. .5204
/organism="Mus musculus"
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s not identified."
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/note="vector:modified
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/clone="mbg11133"
                                                                                                                                                                                              Mus musculus mRNA for mKIAA
AK171132
AK173132.1 GI:50510848
FLI CDNA.
Mus musculus (house mouse)
                                                                 3121 AAAAGTTAAATTTTAAAAA 3139
                                        AAAAGTTAAATTTTGAAAA 5597
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OFAFSYFYTMSAVQPLNISQVFHEVUTDQSGVLSDREIRTLATRIHDLFLSLQDLTG
LEHMLINGSRMLPANITQLNNIPPTQBAYDPNLPPVTKSLVTNCKRVTDKTHKAYKD
KNYRREIDMOBEBIAFWAIRTNVSHVVQQLDDIRKNPRKFVCLNDNIDHNHKDARTVK
AVLRDFYESWFPIIPSQFELDREYRRRFHHHHELQEWRAYRDKLKFWTHCVLATLIIFT
IFSFPAEQIIALKRKIFPRRRIHKBASPDRIRV" KELVPGRRLQQNYFGFLPWEKKKYFQDLLDEEESLKTQLAYFTDSKHTGRQLKDTFAD SLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVNQELQDMFPEEFDKTSFHKVRHSEDM

19; 218 278 338 398 458 121 181 241 518 TACACCTGGGTGAATGGCACTGACCTTGAACTGCTAAAGGAGCTACAGCAGGTCCGAGAG 301 CACATGGAGGAAGAGCGAGGCCATGCGGGAAACCCTCGGGAAGAACACACAACGAACCG 578 61 GGGGTGATGCTGATGCTCCTGCAGAGACAGACCTATACCTGCCTATCCCACAGGTAT GGGCTCTACGTCTGCTTCGTGGGCGTCGTTGTCACCATCGTCTCGGCTTTCCAGTTCGGA GAGGTGGTTCTGGGATGGAGCCGAGATCAGTACCATGTTTTGTTTTGATTCCTACAGAGAC AATATTGCTGGAAAGTCCTTTCAGAATCGGCTTTGTCTGCGCGCATGCCGATTGACGTTGTT Acarrecressaaarecrirreasaaresserersrerseceareseaaresserr TACACCTGGGTGAATGGCACAGATCTTGAACTACTGAAGGAACTACAGCAGGTCAGAGAA CAGATGGAGGAGGAGCAGAAAGCAATGAGAGAAATCCTTGGGGAAAAACACAAGGAACCCT CAAGCTCCTGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTAT **ACTAAGAAGAGTGAGAAGCAGTTAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATG** Gaps DB 10; Length 5204; 128; 814; Indels Score 2874.6; I Pred. No. 0; 0; Mismatches ; 0 51.4%; larity 79.6%; Conservative (

421 638 481 698 critericideaccecececereceaeceaeceaecereaaeearereceaaecerriar CCTTCTTTTCATTCTGCCAGTGACATTTTCAATGTTGCAAAAACCAAAAACCCTTCTACC CITGIACTGGACCCAGCCCTGCCAGCCAACATCACCCTGAAGGACGTGCCATCTTTAT

541 758 

759 CTTAAAGGAAATAGCAGACAGACAGTATGGAGGGGGTACTTGACAACAACAGATAAAGAAGTC

818

661 878 721

601

TTTPAGGGAGGCAGCAACAGATGGTTTGGAGAGCCTACTTGACAACAGACAAAGAAGCC CCTGGATTAGTGCTAATGCAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAG CCTGGCTTAGTGCTGATGCAAGGCTTGGCGTTCCTGAGTGGATTCCCACCGACCTTCAAG

CAGTIGIATICAGAGGCCAGIGIAGCGCTICIAAAACIGAATAACCCCAAGGATTTICAA 998 GAGACGAGTCAACTGAAGACAAAGCTGCCAGAAAAGCTTTCCTCTAAAATAAAGCTGTTG GAAACAAATCAACTAAAAACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTG ceecrgracrccaaeccagrercecrcrrcrcaaarrcaarraarcccaaegerrrccaa

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	AR300468 LOCUS AR300468 LOCUS DEFINITION Sequence 16 from patent US 6537785. ACCESSION AR300468 VERSION KEYWORDS SOURCE Unknown. Unclassified. Unclassified. AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS I (bases 1 to 5229) AUTHORS AUTHORS I (bases 1 to 5229) AUTHORS AUTHORS I (bases 1 to 5229) AUTHORS AUTHORS I (bases) I (base 1 to 5229) AUTHORS AUTHORS I (base 1 to 5229) AUTHORS AUTHORS I (base 1 to 5229) AUTHORS AU	Query Match         50.4%;         Score 2820.8;         DB 6;         Length 5229;           Best Local Similarity 79.1%;         79.1%;         Pred. No. 0;         3           Matches 3667;         Conservative 1;         1;         Mismatches 833;         Indels 137;         Gaps 21;           Qy         150         GGCGGTGAAGGGTGATGCTTTCAAGCTCCTGCAGAGACAAACCTATACCTGCCTG	Oy 210 CACAGGTATGGGCTCTACGTGTGCTCTTGGGCGTCGTTGTCACCGTCTCCGCCTTC 269
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	2452 AGATTGGCCCAGCCTACACTAGGCGTGACTGTGTCCAAAGAGAAC 2667 CCCCCATGTGATTGTTCCACTGGAAAGCCAGATGACAAAAAAAA	CTTTCACCGCTGATCGTTCCCCCGGAAAGCCACT AAAGAAAAAGAGAACAGTAGAATGGAGGAAAATG 	2557 GCAGAA	2847 GAGAAAAAAGTATTTCCAAGATCTTCTCGACGAAGAAGAGTCATTGAAGACACATTG 2847 GAGAAAAAAAGTATTTCCAAGATCTTCTCGACGAAGAAGAGTCATTGAAGACACAATTG	2938 GAGARAMARAGIATIICCARGACCIICIIGAIGAGGAGGGICAIIGAGGAGACCCAGIIG 2907 GCATACTTCACTGATAGCAAAATACTGGGAGGCAACTAAAAAGATACATTTGCAGATTCC 2698 GCGTACTTTACAACTGAAAAAAAAAAAAAAAAAAAAAAA	2967 CTCAGATATGTAAATTCTAAATAGCAAGTTTGGATTCACATCGGAAAGTCCCT 21067 CTCAGATATGTAAATTCTAAATAGCAAAGTTTGGATTCACATCGGAAAGTCCCT 2268 CTCCGATACGACAAATTCTCAAAAATCTCAAGAAAGTTCAAAAAATTCAAGAAAATTCCAAGAAAGTTCAAGAAAATTCAAGAAAATTCCAAGAAAATTCCAAGAAAATTCAAGAAAATTCAAGAAAAATTCAAGAAAATTCAAGAAAATTCAAGAAAATTCAAGAAAATTCAAGAAAATTCAAGAAAATTCCAAGAAAATTCAAAAAATTCAAAAAATTCAAAAAATTCAAAAAA	3027 GCTCACATGCCTCACATGATTGATTGTTATGCAAGAACTGCAGAATGTTCCCT	3087 GAAGAATTTGACAAGACGTCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCC	2878 GAAGAATTIGACAAGACITCATTICACAAAGGGGGGCACTCTGAGGACAIGCAGTITGCC 3147 TTCTCTTATTTATTATCTCATGAGTGCAGTGCAGCCACTGAATATATCTCAAGTCTTT 0000	3207 GATGAAGTTGATACAGATCAGTGCTTGTCTGACACACCCCCCCC	2598 CALGARGIAGACARAGACCARILIGGIGICIIGICIGARAGGARARAICGARACACACACACACACACACACACACACACACACACAC	3327 ATAAATTGCTCAAAAAGCTTCCTGCTGAATATCACGCAGCTAAATAATATTCCACCAACT	3187 CAGGATICTACTATGATCCCACCGCTACTACTCCCAACATCCCACCACT	31/8 CAGGAAGCATACTACGACCCCAACCTGCCTCCGGTCACTAAGAGTCTTGTCACCAACTGT 3447 AAACCAGTAACTGACAAAATCCACAAAAGCATATAAGGACAAAAAAAA	3238 ANGCLAGIAALIGALAAGAICCRAAAGCLIAIARAGALAAGAALAAGAAIACAGIIIGAA 3507 ATCATGGGAGAAAAGAAAAGCGCTTTTAAAATGATTCGTACCAACGTTTCTCATGTGGTT  1007	3230 AICHIGGGARGAGAGAGAGAGAICGCIIICANGAGAGAGAGACGAACGAACGAAGAGAGAGAGAGAGAG	3358 GGTCAGTTGGATGACATCAGAAAAACCCCAGGAAGTTCGTTTGTCTGAATGACATTT 3627 GACCACAATCATAAAGATGCTCAGACAGTGAAGGCTGTTCTCAGGGACTTCTATGAATCC

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November 21, 2004, 18:18:51; Search time 2385 Seconds (without alignments) 12319.082 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-023-888-3 5597 1 cggagccgagcgggcgtccg......aaaaagttaaattttgaaaa 5597 Title: Perfect score:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

4134886 seqs, 2624710521 residues Searched:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Acc81001 H	ADD27811 AAD62491 Human AAD62491 Aad62491 Human	20	6	AAD41203 Aad41203 Human	ACC81010 Acc81010 Human	ACC81011 Acc81011 Human	ADD27809 Add27809 Soluble	AAD62490 N-acetylg	AAD62649 AAD62649 N-acetylg	ACC81007 Acc81007 Murine G	ADD27816 ADD27816 GlcNAc-ph	AAD62493 Mouse cDN	AAD62652 Mouse	ADG39793 Human	ABX10235 Human	ADA53185 Auman	AAL50831 Human	AAH14758 Human	100000
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1716.4	1716.4	1105.2	1104.8	1104.8	1104.8	1104.8	1104.8	1104.8	1103.4	1103.4	1103.4	1103.4	1103.4	1103.4	724.8	692	501	486.2	415.4	398.4	377.2	356:2	353.4
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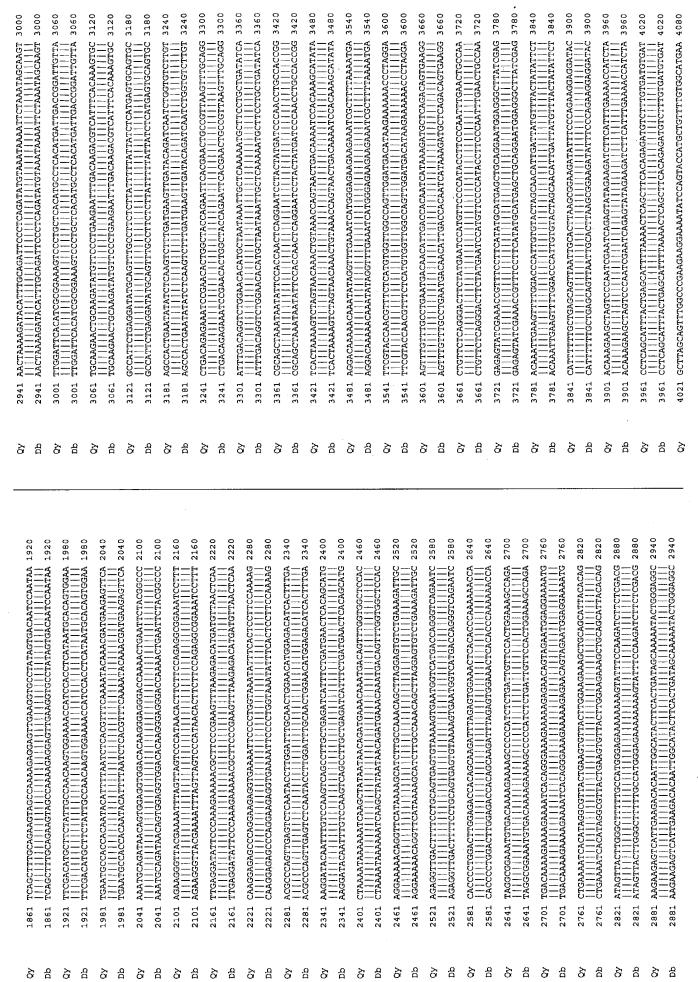
## ALIGNMENTS

Human; N-acetylglucosamine-1-phosphotransferase; nephrotropic; GlcNAc-phosphotranferase; phosphodiester alpha-GlcNAcase; exerviglucosaminidase; bracetylglucosaminidase; enzyme replacement therapy; phosphorylated lysosomal hydrolase; lysosomal storage disease; enzyme; alpha-subunit; gene; ss; beta-subunit. Novel N-acetylglucosamine-1-phosphotransferase and N-acetylglucosamine-1-/\*tag= a /product= "GloNAc-phosphotransferase alpha subunit" /product= "No stop codon given" 2949. .3935 /\*tag= b /\*tag= b /product= "GloNac-phosphotransferase beta subunit" /note= "No start codon" Human GlcNAc-phosphotransferase alpha/beta-subunit cDNA. (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC. Location/Qualifiers ACC81001 standard; cDNA; 5597 BP. 10-AUG-2000; 2000US-00636077. 99US-0153831P. WPI; 2001-290356/30. P-PSDB; ABR61376, ABR61377. (first entry) 14-SEP-1999; Homo sapiens US6537785-B1 Canfield WM; 01-AUG-2003 25-MAR-2003. ACC81001; RESULT 1 ACC81001 CDS 

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                                                                                         The invention relates to a novel isolated human N-acetylglucosamine-1-phosphotransferase (GlcNAc-phosphotranferase) (I) and phosphodiester alpha-GlcNAcase (N-acetylglucosamine-1-phosphodiester alpha-N-Actylglucosaminidase) (II). The protein of the invention has nephrotropic activity, and may be useful in enzyme replacement therapy. A protein of the invention (I), (II) is useful for preparing a protein of the invention (I), (II) is useful for preparing a comprising a terminal mannose-6-phosphate, is useful for treating a patient suffering from a lysosomal storage disease. The present sequence is used in the exemplification of the invention
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 phosphodiester alpha-N-Acetylglucosaminidase, useful for producing phosphorylated lysosomal hydrolase for treating lysosomal storage
                                                                                                                                                                                                                                                                          Sequence 5597 BP; 1678 A; 1151 C; 1219 G; 1549 T; 0 U; 0 Other;
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8 &



Section 2015

	Db 5101 TGCAGTGGCCAATCTCAGCTCACCACCTCCGCCTCCGGGTTCAAGCAGTTCTGTC 5160  Cy 5161 TCAGCCTTCTGAGTAGCTGGGACTACAGGCGTCACACCCTGCTAATTTTTGTA 5220  Db 5161 TCAGCCTTCTGAGTAGCTGGGACTACAGGCGACCCCACACCCTGCTAATTTTTTTT
4561 ATTGACATCTGAAATGCTTTGTAATTATTGACCTCCTAAGAATGCTATGATTTCA 4620	RESULT 2 ADD27811 ID ADD27811 standard; cDNA; 5597 BP. XX AC ADD27811;
4621 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	DT 15-JAN-2004 (first entry) XX XX DE Human GlcNAc-phosphotransferase alpha/beta subunit precursor cDNA. XX KW human, protein phosphorylation; soluble GlcNAc-phosphotransferase; KW human; protein phosphorylation; soluble GlcNAc-phosphotransferase; KW Gene. XX KM Gene. XX KM Gene.
CTCAGTTGGTTTTTGATAGAACAGAGCCAGCAAACTTTCTTGTAAAAGGCTGGTTAGT [	Key CDS CDS
	US2003119088-A. 26-JUN-2003.
4981 ACTGCCCACCAGATGTGACCCTCAGGCCATCATTTGCCAATCACTGAGAATTATT 5040 5041 ITGTTGTTGTTGTTGTTTTTTAGACACAGACTCTCTCTCTC	XX PF 21-DEC-2001; 2001US-00023888. XX XX PR 21-DEC-2001; 2001US-00023888. XX
	(NOVA-) NOVAZIME FRAKM Canfield W, Kudo M;

Phosphorylating a protein for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease by contacting the protein with a soluble GlcNAc-phosphotransferase and producing a phosphorylated WPI; 2003-801323/75. P-PSDB; ADD27812, ADD27813. ID NO Disclosure; SEQ protein. RRXFFFFXXXX00000

The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble GlcNAc-phosphotransferase (UDP-N-acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering Irom a lysosomal storage disease e.g. Fabry's disease. The present sequence represents the human GlcNAc-

English

3; 55pp;

383	e.g. rabry's d phosphotransfe	qisease. The present sequence represents the numan GichAc- erase alpha/beta subunit precursor cDNA.
SOS	Sequence 5597	BP; 1678 A; 1151 C; 1219 G; 1549 T; 0 U; 0 Other;
B Q	uery Match est Local Simila	100.0%; Score 5597; DB 10; Length 5597; 100.0%; Pred. No. 0;
Ma	5597; (	ive 0; Mismatche
ò	1 CGGAG	CGGAGCGGAGCGGCGTCCGTCGCCGGAGCTGCAATGAGCGGCGCCCCGGAGGCTGTGACC 60
qq		ccaaccacatcarcarcacadaacracaaraadacacaccadaadaraacc 60
δλ	61 TGCGC	TGCGCGCGCGCGCCCCGGGGCCCCCTGAATGGCGGCTGAGGCGGCGGCGGCGGCGC 120
QQ	61 TGCGC	gagacagacacagacacacacacacacacacacacacac
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ò	181 TGCAG	TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240
9 <u>0</u>	181 TGCAG	AGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240
ολ	241 GCGTC	GCGTCGTTGTCACCATCGTCTCCGCCTTCCAGTTCTCGAGAGGTGGTTCTGGAATGGAGCC 300
q	241 GCGTC	GTTGTCACCATCGTCTCCGCCTTCCAGTTCGGAGAGGTGGTTCTGGAATGGAGCC 300
δ	301 GAGAT	GAGATCAATACCATGTTTGTTTGTTTGTTTGTAGAGACAATATTGCTGGAAAGTCCTTTC 360
d G	301 GAGAT	CAATACCATGITITGITIGATICCIATAGAGACAATATIGCIGGAAAGICCITIC 360
δ	361 AGAAT	AGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGATGGCACAG 420
QQ	361 AGAAT	CGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG 420
δλ	421 ATCTT	TITITI TITIT
qq	421 ATCTT	GAACTACTGAAGGAACTACAGCAGGTCAGAGAACAGATGGAGGAGGAGGAGCAGAAAG 480
ò	481 CAATG	CAATGAGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAAGCAGT 540
QQ .	481 CAATG	AGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAAGCAGT 540
ò	541 TAGAG	TAGAGIGITIGCIAACACACIGCATTAAGGIGCCAAIGCITGTACIGGACCCAGCCCTGC 600
QQ	541 TAGAG	TGTTTGCTAACACCCCCATTAAGGTGCCAATGCTTGTACTGGACCCAGCCCTGC 600
δλ	601 CAGCC	CAGCCAACATCACCCTGAAGGACGTGCCATCTTTATCCTTCTTTTCATTCTGCCAGTG 660
qq	601 CAGCC	AACATCACCCTGAAGGACGTGCCATCTCTTTATCCTTCTTTTCATTCTGCCAGTG 660
Š	661 ACATT	ACAITITCAAIGITGCAAAACCAAAAACCCITCTACCAATGICTCAGITGITGITITG 720
QQ	661 ACATT	TICAAIGIIGCAAAACCAAAAACCCIICIACCAAIGICICAGIIGIIGIIIIIG 720
ò	721 ACAGT	ACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGACAGA

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1320 1200 1260 1500 1020 1080 1200 1320 1380 1380 1500 1560 1620 1680 1020 1860 840 840 900 960 CAGTATGGAGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAG AATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCTGCTGTTTCAGAGGCCAGTG AGAACATGACCATTGATGAAGAAAGAACTGACCATAAGTCCTGCATATTATTATGGGGATC TGAGCGCCATCAGCCGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAAGATA ACGAAGAACTGAGGTACTCATTGCGATCTATCGAGAGGCATGCACCATGGGTTCGGAATA TTTTCATTGTCACCAACGGGCAGATTCCATCCTGGCTGAACCTTGACAATCCTGAGTGA TGAGCGCCATCAGCCAGCTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAAGATA ACGAAGAACTGAGGTACTCATTGCGATCTATCGAGGGCATGCACCATGGGTTCGGAATA TITICATIGICACCAACGGGCAGATICCAICCIGGCIGAACCIIGACAAICCIGGAGIGA CAATAGTAACACCAGCAGGATGTTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGTTCAC ATGATGATGTTTGGGAAGGAAGTGTCTGGCCAGATGATTTTACAGTCACTCCAAAG ATGATGATGTCATGTTTGGGGAAGGATGTCTGGCCAGATGATTTTTACAGTCACTCCAAAG GCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAGGGCTGCCAGGTTCCT CAGTATGGAGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAG ATTIGGCTTTCCTGAGTGGATTTCCACCACCACTTCAAGGAAACAAATCAACTAAAAACAA AGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATGGGATC CAATAGTAACACCAGGATGTTTTTCGAAATTTGAGCCACTTGCCTACCTTTAGTTCAC GCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAGGCTGCCCAGGTTCCT TGTCCTGTGGGTTTGATGCTGGCGACTGTGGGCAAGATCATTTTCATGAATTGTATAAAG TGTCCTGTGGGGTTTGATGCTGGCGACTGTGGGCAAGATCATTTTCATGAATTGTATAAAG 1741 1021 1021 1081 1081 1141 1141 1201 1201 1261 1261 1321 1321 1381 1381 1441 1441 1501 1501 1561 1561 1621 1621 1681 721 781 841 901 901 961 1681 1741 1801 1801 781 841 961 8 & B 8 B 8 8 & 8 8 8 8 90 % PG 8 8 8 8 6 6 QC ò g 8 8 ò g ò

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5 8 8 8	AAATGCAGATAACAGTGGAGGTGGACACAAGGGAGGGACCAAAACTGAATTCTACGGCCC AGAAGGGTTACGAAAATTTAGTTAGTCCCATAACACTTCTTCCAGAGGGGAAATCCTTT AGAAGGGTTACGAAAATTTAGTTAGTCCCATAACACTTCTTCCAGAGGGGGAAATCCTTT AGAAGGGTTACGAAAATTTAGTTAGTCCCATAACACTTCTTCCAGAGGCGGAAATCCTTT	43	decarrerdadadatatecarrigecriterertatritatratererargaergecarge a accentrergadadatatererargergecarge a accentrer a accentraterargament and the second and accentrate a accentrat
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) & A &	ACGCCCAGTTGAGTCTCAATACCTTGGATTTGCAACTGGAACATGGAGACATTGA 	S a S	CGCAGCTAAATAATTCCACCAACTCAGGAATCCTACTATGATCCAACCTGCCACGG
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8 8 8	2461 AGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGATTGC 2520	& A & &	3541 TTGGTACCAACGTTTCTCATGTGGTTGGTTGGATGATGAAAAAACCCTAGGA 3500 3541 TTGGTACCAACGTTTCTCATGTGGTTGGCCAGTTGGATGATAAGAAAAAACCCTAGGA 3600 3601 AGTTTGTTGCCTGAAGAACAACATTGACCACAATCATAAGAAAAAACCCTAGGA 3600 3601 AGTTTGTTTGCCTGAAGAACAACATTGACCACAATCATAAAAAAAA
<b>9</b> 6 9	2521 AGAGGTTGACTTTTCCTGGAGTGAGTGAAAGTGACGTCATGACCAGGGTCAGAATC 2580 2581 CACCCCGGACTTGGAGACCAGCAAGATTTAGAGTGGAAACTCACACCCAAAAAACCA 2640 2581 CACCCCTGGACTTGGAGACCAGCAAGATTTAGAGTGGAAACTCACACCCAAAAAACCA 2640 2581 CACCCCTGGACTTGGAGACCACAGCAAGATTTAGAGTGGAAACTCACACCCAAAAAACCA 2640	9 & 9 6 & 6	CIGITATICAGE CITCAGA CONTROL C
65 d	TAGGCGGAAATGTGACAAAAGAAAAGCCCCCATCTCTGATTGTTCCACTGGAAAGCCAGA 270	8 8 8	3721 GAGAGTATCGAAACCGTTTCCTTCATATCCTTCAACCTGCAGGAATGGAGGCTTATCGAG 3780 3721 GAGAGTATCGAAACCGTTTCCTTCATATCCATGGAGGAATGGAGGCTTATCGAG 3780 3781 ACAAATTGGAGCCCATTGTGTACTAGGAACAATTGGATTACCTATATCTTATGTTTACTATTATTTTT 3840
\$ 6 B 6	2701 TGACAAAGAAAATCACAGGGAAAGAAAAAGAGAACAGTAGAATGGAGGAAAATG 2760 2701 TGACAAAAGAAAGAAAATCACAGGGAAAGAAAAGAAAAG	දුර රථ	3781 ACAAATTGAAGTTTTGGACCCATTGTGTACTAGCAACATTGATTATGTTTACTATATTCT 3840 3841 CATTTTTGCTGAGCAGTAATTGCACTTAAGCGGAAGATATTTCCCAGAAGGAGGATAC 3900 3841 CATTTTTGCTGAGCAGTTAATTGCACTTAAGCGGAAGATATTTCCCAGAAGATAC 3900
3 & 3	ATAGITACTTGGGCTTTTTGCCATGGGAAAAAAAGTATTTCCAAGATCTTCTGACG 288 ATAGITACTTGGGCTTTTTGCCATGGGAAAAAAAAAATATTTCCAAGATCTTCTCGACG 288 ATAGITACTTGCCTTTTTGCCATGGGAAAAAAAAAATATTTCCAAGATCTTCTCACG 288	QV DP	396
oy da	2881 AAGAAGAGTCATTGAAGACACAATTGGCATACTTCACTGATAGCAAAATACTGGGAGGC 2940 	çy Ob	3961 CCTCAGCATTTACAGAACTCAGCAGAGATGTCTTTTGAGAGATGTTTTGAT 4020

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                                                                                                                                                                                                                                         The invention relates to a method for producing a high mannose glycoprotein. The method comprises: introducing and expressing a polynucleotide encoding a glycoprotein into a mammalian cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of decoymannojirinycin and kifunensine to inhibit glycosylation of the glycoprotein; and collecting the glycoprotein. The invention is useful in gene therapy. The method is useful for producing a high mannose lycoprotein in a complex carbohydrate deficient cell for treating lysosomal storage disease. The present sequence is human N-acetylglucosamine-1 (GLCNAc)-phosphotransferase alpha/beta subunit
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                                                                                                                                 Producing a high mannose glycoprotein for treating lysosomal storage disease, comprises culturing the lectin resistant mammalian cell in t presence of deoxymannojirimycin and kifunensine.
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Matches 5597; Conservative 0; Mismatches
                                                                                                                                                                                                             Claim 12; Page 13-15; 46pp; English.
                                                                                                       P-PSDB; ABW01488, ABW01489
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                                                                                       2003-810984/76.
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                                                                                                                                                                                 Producing a glycoprotein with reduced complex carbohydrates by culturing
the lectin resistant mammalian cell expressing the glycoprotein for
                                                                                                                                                                                                                                                                                                                                            Sequence 5597 BP; 1678 A; 1151 C; 1219 G; 1549 T; 0 U; 0 Other;
                                                                                                                                                                                                                               Claim 12; Page 13-15; 46pp; English
                                                                                                                                                                                                        treating lysosomal storage disease.
                                                         21-DEC-2001; 2001US-00023890.
                                                                               21-DEC-2001; 2001US-00023890.
                                                                                                                                               WPI; 2003-810985/76.
P-PSDB; ABW01537, ABW01538
                                                                                                    (NOVA-) NOVAZYME PHARM INC
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1621	GTATTGGAGTTGGACACCCCTGGCAGTTTGGTGGAGAATAAACAGTGTCTCTTACTGTA 1680 ATCAGGAIGTGGGAATTCCTGGCTCGCTGATAAGTTCTGTGACCAAGCATGCAATGTCT 1740	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	2761 CTGAAAATCACATAGGCGT 
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2281 ACG     2281 ACG	ACGCCAGTTGAGTCTCAATACCTTGGATTTGCAACTGGAACATGGAGACATCACTTTGA 2340 	<b>상</b> 원	361 CGCAGCTAAAT            361 CGCAGCTAAAT
2341 AAGGAT7        2341 AAGGAT7	GATACAATTIGTCCAAGTCAGCCTTGCTGAGATCATTTCTGATGAACTCACAGCATG 2400 ·	රු දු	421 TCACTAAAAC            421 TCACTAAAAC
2401 CTAAAA:        2401 CTAAAA:	aaataaaaatcaagctataataacagatgaaacaaatgacagtttggtggctccac 2460 	y d	481 AGGACAAAACAAAT 
2461 AGG     2461 AGG	AGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGATTGC 2520 	λ da	
2521 AGA     2521 AGA	AGAGGITGACTITICCTGCAGTGAGTGAAAGTGAATGGTCATGACCAGGGTCAGAATC 2580	රු පු	3601 AGTTTGTTTGCCTGAATGAC 
	0 0	ço da	CTGTTCTC 
2641 TAGO      2641 TAGO	TAGGGGAAATGTGACAAAAGAAAGCCCCCATCTCTGATTGTTCCACTGGAAAGCCAGA 2700 	y da	
2701 TGACAAA         2701 TGACAAA	baargaaaargaaaatcacaggaaagaaaaaaagaaacagtagaatggaggaaatg 2760 		3781 ACAAATTGAAGTTTTGGACC 

2820 2880 2880 AAGTCCCTGCTCACATGCCTCACATGATTGACCGGATTGTTA 3060 3180 CCCATTGTGTACTAGCAACATTGATTATGTTTACTATATTCT 3840 CAGATTCCCTCAGATATGTAATAAAATTCTAAATAGCAAGT 3000 AGTTTGCCTTCTCTTATTTTATTATCTCATGAGTGCAGTGC 3180 AAGTCTTTGATGAAGTTGATACAGATCAATCTGGTGTCTTGT 3240 ACCAACTCAGGAATCCTACTATGATCCCAACCTGCCACGG 3420 INDICATION OF THE CONTROCT TO THE CONTROL OF THE CONTROL OF THE CONTROCT OF THE CONTROL OF THE CONTROC OF THE CONTROL OF THE C CCTTCATATGCATGAGCTGCAGGAATGGAGGCCTTATCGAG 3780 AGATICCCICAGATAIGTAAATAAAATICTAAATAGCAAGT 3000 AGTCTTTGATGAGTTGATACAGATCAATCTGGTGTCTTGT 3240 CATGCTAATAAATTGCTCAAAAATGCTTCCTGCTGATATCA 3360 CATGCTAATAAATTGCTCAAAAATGCTTCCTGCTGATATCA 3360 GGTTTGAAATCATGGGAGAAGAAGAAATCGCTTTTAAAATGA 3540 GETTTGAAATCATGGGAGAAGAAGAAATCGCTTTTAAAATGA 3540 ATGTGGTTGGCCAGTTGGATGACATAAGAAAAAACCCTAGGA 3600 ACTGGCTACCAGAATTCACGAACTGCCGTTAAGTTTGCAGG 3300 AAACTGTAAACCAGTAACTGACAAAATCCACAAAGCATATA 3480 ACAACATTGACCACAATCATAAAGATGCTCAGACAGTGAAGG 3660 TACTGAAGTGTTACTTGGAAGAAAGCTGCAGCATTACACAG TACTGAAGTGTTACTTGGAAGAAGCTGCAGCATTACACAG IGCCATGGGAGAAAAAAAGTATTTCCAAGATCTTCTCGACG ACAATTGGCATACTTCACTGATAGCAAAAATACTGGGAGGC 

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                                                                      CAGAGAACAGATGGAAGAAGGAGGAAGCAATGAGAAATCCTTGGGAAAAACACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acid-associated proteins (NAAP) and nucleic acids and amino acid sequences are useful for diagnosing, treating and preventing cell proliferative e.g. arteriosclerosis, atherosclerosis, lymphoma or cancers), neurological (e.g. epilepsy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. ALDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful igene therapy. The present sequence is human NAAP-9 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS).
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                                                                                               21-DEC-2000; 2000US-0257714P.
05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262302P.
23-JAN-2001; 2001US-0263823P.
02-FBB-2001; 2001US-0266088P.
29-OCT-2001; 2001US-0348442P.
                                                            19-DEC-2001; 2001WO-US050256
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P-PSDB; AAE25290.
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                      27-JUN-2002
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2612 TAGAGTGGAAACTCACACCCAAAAACCATAGGCGGAAATGTGACAAAAGAAAAGCCCCC 2671 	2672 AICTCTGATTGTTCCACTGGAAAGCCAGATGACAAAAGAAAAATCACAGGGAAAGA 2731 	2732 AAAAGAGAACAGTAGAATGGAGAAAATGCTGAAAATCACATAGGCGTTACTGAAGTTT 2791 	GAAAGCTGCAGCAITACACAGATAGTTACTTGGGCTTTTTGCCATGGGAGAA 285 	852 AAAAAGTATTTCCAAGATCTTCTCGACGAAGAAGAGTCATTGAAGACACAATTGGCATA 2 	912 CTTCACTGATAGCAAAAATACTGGGAGCAACTAAAAATACATTTGCAAATTCCTCAG 297 	972 ATATGTAARTAAANTTCTAAATAGCAAGTTTGGNTTCACATCGCGGAAAGTCCTGCTCA 30 	032 CATGCCTCACATGATTGACGGGATGTTATGCAAQAACTGCAAGATATGTTCCCTGAAGA 30 	92 ATTIGACAAGACGTCATITCACAAAGIGGGCCATICTGAGGATAIGCAGTITGCCTICTC 3 	152 TTATTTTATTATTATCTCATGAGTGCAGCGCACTGAATATATCTCAAGTCTTTGATGA 321 	SCTACCAG 327          SCTACCAG 324	rcacgaactgccgttaagtttgcaggatttgacaggtctggaacacatgctaataaa 333 	SCAGCTAAATAATATTCCACCAACTCAGGA 33 	392 AICCTACTATGAICCCAACCTGCCACGGICACTAAAAGICTAGIAAACTGIAAACC 345 	452 AGTAACTGACAAAATCCACAAAGCATATAAGGACAAAAAACAATTATAGGTTTGAAATCAT 351 	357	batgacataagaaaaaccctaggaagtitgttigcctgaatgacaacattgacca 36 	3632 CAATCATAAAGATGCTCAGACAGTGAAGGCTGTTCTCAGGGACTTCTATGAATCCATGTT 3691 	VTACCTTCCCAATTTG	
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1532 TAATAATTCAGCCTGCGATTGGGATGGTGGGGATTGCTCTGGAAACAGTGGAGGGAG	592 CIATATICAGAGGGGAGGAGGAGGAGGAGTTGGAGTTGGAGACACCCCTGGCAGGGTTGG 165  6. IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		712 TAAGTTCTGTGACCAAGCATGCAATGTCTTGTGGGTTTGATGCTGGGGGTT70	72 GCAAGATCATTTTCATGAATTGTATAAAGTGATCCTTCTCCCAAACCAGACTCACTATAT 1	aaaggtgaatgcctgccttatttcagctttgcagaagtagccaaaaga( 	rggaa 19       rggaa 19	rccacctcataatgcacagtggaatgaatgccaccacaatacattttaatctcac 20 	012 GTTTCAAAATACAAACGATGAAGAGTTCAAAATGCAGATAACAGTGGAGGTGGACACAAG 20 	2072 GGAGGGACCAAAACTGAATTCTACGGCCCAGAAGGGTTACGAAAATTTAGTTAG	AAATCCTTTTGAGGATATTCCCAAAGAAAAACGC 	92 GAAGITITAAGAGACAIGAIGITIAACICAACAAGGAGAGGCCAGGAAGAGGICAAAAITCC 225 		312 GCAACTGGAACATGGAGACATCACTTTGAAAGGATACAATTTGTCCAAGTCAGCCTTGCT 237	articigaigaactcacagcafgctaaaataaaaatcaagctataata 		92 AAACAGCTTAGGAGTGTCTGAAAGATTGCAGAGGTTGACTTTTCCTGCAGTGAGTG	552 AGTGAATGGTCATGACCAGGGTCAGAATCCACCCCTGGACTTGGAGACCACAGCAAGATT 261	gaatggtcatgaccagggtcagaatccaccctggacttggagaccacgcaaga	

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ITCCTATAGAGACAATATTGCTGGAAAGTCCTTTCAGAATCGGCTTTGTCTGCCCATGCC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS).
                                                                                                                                                                                                                                                                                                                  Baughin MR, Lu Y, Arvizu C, Ramkumar J, Yao MG, Policky JL;
Walia NK, Tribouley KM, Yue H, Barra S, Ding L, Lal PG;
Borowsky ML, Lu DAM, Gandhi AR, Griffin JA, Xu Y, Azimzai Y;
Gierzen Ky, Tng YT, Warren BA, Mason PM, Burford N, Hafalia AJA;
Lee EA, Yang J, Gorvad AE, Emerling BM, Marquis JP, Lee SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acid-associated proteins (NAAP) and nucleic acids. The nucleic acid and amino acid sequences are useful for diagnosing, treating and preventing cell profiferative e.g. arteriosclerosis, atherosclerosis, lymphoma or cancers), neurological (e.g. epilepsy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. AIDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania) as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GAAGCTGCAATGAAGCGGCGCCGGAAGCTGTGACCTGCGCGCGGCGGGGCCCGACCGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4277 BP; 1325 A; 891 C; 925 G; 1135 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 4277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene therapy. The present sequence is human NAAP-13 cDNA
                            /product= "Mature human NAAP-13"
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                                                                                                                                                                  21-DEC-2000; 2000US-0257714P.
05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262302P.
23-JAN-2001; 2001US-0263823P.
02-FEB-2001; 2001US-0266081P.
29-OCT-2001; 2001US-0348442P.
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Best Local Similarity 95.7%;
Matches 4264; Conservative
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243. .3728
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P-PSDB; AAE25294.
                                                                   WO200250279-A2
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                 CCCCATACCTTCCCAATTTGAACTGCCAAGAGTATCGAAACCGTTTCCTTCATATGCA 3720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, nucleic acid-associated protein, NAAP-13; neurological disorder, arteriosclerosis, cancer, cell proliferative disorder; atherosclerosis; lymphoma; epilepsy, Alzheimer's disease, developmental, articonvulsant, autoimmune disorder; AIDS; allergy; anamia; stroke; malaria; leishmania; gene therapy, nootropic; neuropprotective; cerebroprotective; virucide; immunosuppressive; protozoacide; antimicrobial; gene; ss.
                                                                                                                                            ACCAACATTGATTATGTTTACTATATTCTCATTTTTTTCCTGAGCAGTTAATTGCACTTAA
                                                                          TGAGCTGCAGGAATGGAGGGCTTATCGAGACAATTGAAGTTTTGGACCCATTGTGTACT
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                                                 TGAGCTGCAGGAATGGAGGCCTTATCGAGACAAATTGAAGTTTTGGACCCATTGTGTACT
                                                                                                                   AGCAACATTGATTATGTTTACTATATTCTCATTTTTTGCTGAGCAGTTAATTGCACTTAA
                                                                                                                                                                                     GCGGAAGATATTTCCCAGAAGGAGGATACACAAAGAAGCTAGTCCCAATCGGAATCAGAGT
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141. .3731
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1382 TGTCTGGCCAGATGATTTTTACAGTCACTCCAAAGGCCAGAAGGTTTATTTGACATGGCC 144	OY 1466 TGTGCCAAACTGTGCCGAGGCCTGCCAGGTTCCTGGATTAAGGATGGCTATTGTGACAA 1525  Db 1442 T	Oy 1526 GGCTTGTAATAATTCAGCCTGCGATTGGGATGGTGGGGGATTGCTCTGGAAACAGTGGAGG 1585 Db 1443 1442	OY 1586 GAGTCGCTATATTGCAGGAGGTGGAGGTACTGGGAGTATTGGAGTTGGACACCCCTGGCA 1645 Db 1443	Oy 1646 GTTTGGTGGAGGAATAAACAGTGTCTTACTGTAATCAGGGATGTGCGAATTCCTGGCT 1705	y 1706 cgctgataagtrctgaccaagcatgcaatgrcttgrccrgtgggtrtgatgctgggg 1765	Y 1766 CIGIGGGCAAGAICATITICAIGAAITGTAIAAAGIGAICCTICTCCCAAACCAGACTCA 1825	y 1826 CTATATTATTCCAAAAGGTGAATGCCTGCCTTATTTCAGCTTTGCAGAAGTAGCCAAAAG 1885	y 1886 AGGAGTIGAAGGIGCCTAIAGTGACAATCCAATAATTGGACATGCTTCTAITGCCAACAA 1945	1946	y 2006 TCTCACGTTTCAAATACAAACGATGAAGAGTTCAAAATGCAGATAACAGTGGA 2065	y 2066.Cacaagggaggaccaaaactgaattctacggcccagaagggttacgaaaatttagttag	2126	2186 CTTCCCGAAGTTTAAGAGACATGATGATAACTCAACAAGAGAGACCCAGGAAGAGGGGAAAAAAAA	2246 AATTCCCCTGGTAATATTCACTCCTTCCAAAGACGCCGAGTTGAGTCTCAATACCTT	2306 GGATTIGCAACTGGAACATGGGAGACATCACTTTGA 	2366	2426	y 2486 CTTGCCAAACAGCTTAGGAGTGTCTGAAAGATTGCAGAGGTTGACTTTTCCTGCAGTGAG 2545
	<del>о</del> А	<i>ኢ</i> 42	ሌ <b>զ</b>	δ d	۸۶ مو	λδ <u></u>	₹ 	δ <sub>0</sub> α	۵۲ مو	ζο Pag	δ dd		do do	λο q <sub>α</sub>	<u>දි</u>	ර් <u>අ</u>	δ 	Да
302 TTCCTATAGAGACAATATTGCTGGAAAGTCCTTTCAGAATCGGCTTTGTCTGCCCATGCC 361	386 GATTGACGTTGTTTACACCTGGGTGAATGGCACAGATCTTGAACTACTGAAGGAACTACA 445 	46 GCAGGTCAGAGAACAGATGGAGGAGGAGCAGAAAGCAATGAGAGAAATCCTTGGGAAAAA 	06 CACAAC	66 TAAGGTGCCAATGCTTGTACTGGACCCAGCCAGCAAGATCACCCTGAAGGACGT	s occarcititatocitititataticidecagidacatititicalgiticaaaaccaaa	1 1	46 CCACTCTGGACTGCTTAAAGGAAATAGCAGACAGACAGTATGGAGGGGGTACTTGACAAC 	AGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAGATTTGGCTTTCCTGAGTGGATTTCC 	6 ACCAACATTCAAGAAACAAATCAACTAAAAACAAAATTGCCAGAAAATCTTTCCTCTAA	AGTCAAACTGTTGCAGTTGTATTCAGAGGCCAGTGTAGGCGCTTCTAAAACTGAATAACCCAGTGTAAACTGAATAACCCAGTGTAGAACTGAAACTGAATAACCCAGTGTAGGGCTTCTAAAACTGAATAACCAAACTGAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAACTGAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAACTGAAAAAACTGAAAAAAAA	86 CAAGGAITITCAAGAATIGAATAAGCAAACTAAGAAGAACATGACCATIGATGAAAAGA	46 ACTGACCATAAGTCCTGCATATTTATTATGGGATCTGAGCGCCATCAGCCGGTCTAAGCA	9 N	1166 ATCTATCGAGAGGCATGCACCATGGGTTCGGAATATTTTCATTGTCACCCAACGGGCAGAT 1225 	1226 TCCATCCTGGCTGAACCTTGACAATCCTCGAGTGACAATAGTAACACACCAGGATGTTTT 1285 	86 TCGAAATTTGAGCCACTTGCCTACCTTAGTTCACCTGCTATTGAAAGTCACATTCATCG 13 	46 CATCGAAGGGCTGTCCCAGAAGTTTATTTACCTAAATGATGATGATGTTTGGGAAGGA 14	6 TGTCTGGCCAGATGATTTTTACAGTCACCCAAAGGCCAGAAGGTTTATTTGAC
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9 16.5 TGATCACALATCATAAAGATGCTCAGACATGAAGGCTGTTCTCAGGGCATTCTTCTCAGATC 3481  9 12.2 TGATCACCACAATCATTCACACCCAGAGAGTGTTCCAGAACATCCAGAGACTTCCTTC	RESULT 7 ACC81010 ID ACC81010 XX AC ACC81010; XX DT (1-AUG-2003 (first entry) XX DE Human GlcNAc-phosphotransferase related cDNA SEQ ID NO: 20. XX
2516 TIGHAMAGTGAATGGCATGACCAGGATCCACCAGGACTGGCACCCAGG 2 605 2312 TIGHAAAGTGAATGCCATGACCAGGACTCACAATCCCCCTGGACTTGGCACCACAGG 2 101 2806 AAGATTTAGATGCAATCCACCAGGACTCACAAAACCCTAGACTGCAAAAAAAA	

N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase; enzyme replacement therapy; phosphorylated lysosomal hydrolase; lysosomal storage disease; gene; ss. (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC 10-AUG-2000; 2000US-00636077 WPI; 2001-290356/30. Homo sapiens 14-SEP-1999; US6537785-B1 25-MAR-2003 Canfield 

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Novel N-acetylglucosamine-1-phosphotransferase and N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase, useful for producing phosphorylated lysosomal hydrolase for treating lysosomal storage diseases.

Example 9; Page 52-54; 62pp; English,

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4 The invention relates to a novel isolated human N-acetylglucosamine-1-phosphotransferase (GlcNAc-phosphotranferase) (I) and phosphodiester Alpha-GlcNAcase (N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase) (II). The protein of the invention has nephrotropic activity, and may be useful in enzyme replacement therapy. A protein of the invention (I), (II) is useful for preparing a protein of the invention (I), (II) is useful for preparing a phosphorylated lysosomal hydrolase. The phosphorylated hydrolase comprising a terminal mannose-6-phosphate, is useful for treating a patient suffering from a lysosomal storage disease. The present sequence is used in the exemplification of the invention

Sequence 3783 BP; 1198 A; 776 C; 835 G; 974 T; 0 U; 0 Other;

224 284 126 186 246 366 344 404 464 306 524 584 426 99 TACGTGTGCTTCTTGGGCGTCGTTGTCACCATCGTCTCCCGCCTTCCAGTTCGGAGAGGTG AAGAGTGAGAAGCAGTTAAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTA AndGGGTTCAAGCTCTTGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTC TACGTGTGCCTTCTTGGGCGTCGTTGTCACCATCGTCTCCGCCTTCCAGTTCGGAGAGGTG GCTGGAAAGTCCTTTCAGAATCGGCTTTGTTCTGCCCATGCCGATTGACTTGTTTACACC TGGGTGAATGGCACAGATCTTGAACTACTGAAGGAACTACAGCAGGTCAGAGAACAGATG GAGGAGGAGCAGAAAGCAATGAGAAAATCCTTGGGAAAAAACACAACGGAACCTACTAAG AAGAGTGAGAAGCAGTTAGAGTGTTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTC GCTGGAAAGTCCTTTCAGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACC CTGGACCCAGCCCTGCCAGCCAACATCACCCTGAAGGACGTGCCATCTCTTTATCCTTCT 6 Length 3783; Indels Match 67.2%; Score 3761; DB 4; Local Similarity 99.7%; Pred. No. 0; les 3767; Conservative 0; Mismatches 10; Query Match Best Local Si Matches 3767; 1 165 225 67 285 127 405 247 345 187 465 307 525 367 ΩD 8 8 8 S B 음 ò 셤 ò 엄  $\delta$ 8 8

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1184 1004 1064 1124 1424 1604 1446 1664 AGTGTCTTACTGTAATCAGGGATGTGCGAATTCCTGGCTCGCTGATAAGTTCTGTGAC 1724 786 846 996 486 764 909 726 944 704 824 999 884 TTTCATTCTGCCAGTGACATTTTCAATGTTGCAAAAACCAAAAAAACCCTTCTACCAAATGTC TCAGTTGTTGTTTTGACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAA GGAAATAGCAGACAGACAGTATGGAGGGGCTACTTGACAACAGATAAAGAAGTCCCTGGA TTAGTGCTAATGCAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAGGAAACA AATCAACTAAAAACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTG TATTCAGAGGCCAGTGTAGCGCTTCTAAAACTGAATAACCCCCAAGGATTTTCAAGAATTG AATAAGCAAACTAAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCA TACAGTCACTCCCAAAGGCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAG CTGGACCCACCCTGCCAGCCAACATCACCCTGAAGGACCTGCCATTATCCTTCT TCAGTTGTTGTTTTTGACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAA TTAGTGCTAATGCAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAGGAAACA AATCAACTAAAAACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTG TATTCAGAGGCCAGTGTAGCGCTTCTAAAACTGAATAACCCCAAGGATTTTCAAGAATTG AATAAGCAAACTAAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCA TATTTATTATGGGATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCC CCATGGGTTCGGAATATTTTCATTGTCACCAACGGGCAGATTCCATCCTGGCTGAACCTT GACAATCCTCGAGTGACAATAGTAACACCCCCGGGATGTTTTTCGAAATTTGAGCCACTTG GGAAATAGCAGACAGACAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGA TATTITATTATGGGATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCC CCATGGGTTCGGAATATTTTCATTGTCACCAACGGGCAGATTCCATCCTGGCTGAACCTT GACAATCCTCGAGTGACAATAGTAACACACCAGGATGTTTTTCGAAATTTGAGCCACTTG CCTACCTTTAGTTCACCTGCTATTGAAAGTCACATTCATCGCATCGAAGGGCTGTCCCAG CCTACCTTTAGTTCACCTGCTATTGAAAGTCACGTTCATCGCATCGAAGGGCTGTCCCCAG AAGTTTATTTACCTAAATGATGATGTCATGTTTGGGAAGGATGTCTGGCCAGATGATTTT TACAGTCACTCCAAAAGGCCAGAAGGTTTATTTGACATGGCCTGTGCCCAAACTGTGCCGAG GGCTGCCCAGGTTCTGGATTAAGGATGGCTATTGTGACAAGGCTTGTAATTCAGCC TGCGATTGGGATGGTGGGATTGCTCTGGAAACAGTGGAGGAAGTCGCTATATTGCAGGA GGTGGAGTACTGGGAGTATTGGACTTGGACAGCCCTGGCAGTTTGGTGGAATAAAC <u> AAGTTTATTTACCTAAATGATGATGTCATGTTTGGGAAGGATGTCTGGCCAGATGATTTT</u> GGTGGAGGTACTGGAGTTTGGACTTGGACACCCCTGGCAGTTTGGTGGAGGAATAAAC 1267 1005 1065 1125 1185 1027 1245 1087 1305 1147 1207 1425 1485 1327 1545 1387 1447 1665 645 487 705 547 165 607 825 667 885 727 945 787 847 907 967 1365 1605 427  $\delta$ g g 8 음 중 음 원 장 원 

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2805 CIGCAGCAITACACAGAIAGTIACTIGGGCITITIGCCAIGGAGAAAAAAAGTAITIT 28 [	2865 CAAGAICTICTICGACGAAGAAGATCATTGAAGACAATTGGCATAACTTGATGACATTGCATGATTGCATGATTGCATGATTGCATTGATGACATTGATGACATTGATGATTGAT	2925 AAAATACTGGGAGGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGAAAA 2 2767 AAGAATACTGGGAGGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGTAAATAA 2	2985 ATTCTAARTAGCAAGTTTGGATTCACATCGCGGAAGTCCCTGGTCACATGCCTCACATG	3045 ATTGACGGATTGTTATGCAAGAACTGCAAGATATGTTCCCTGAAGATTTGACAAGAACG 31 2887 ATTGACGGATTGTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGACAAGACG 29	3105 TCATTTCACAAAGTGCGCCATTCTCAGGATATGCATTGCCTTCTTATTTTTATTAT 31 2947 TCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTCTTATTTTTTTATTAT 30	3165 CTCATGAGTGCAGTGCAGCCACTGAATATATCTCAAGTCTTTGATGAGTTGATACAGAT 32 3007 CTCATGAGTGCAGTGCAGCCACTGAATATATCTCAAGTCTTTGATGAAGTTGATACAGAT 30	CTACCAGAATTCACGAACTG 3	3285 CCGTTAAGTTTGCAGGATTTGACAGGTCTGGAACACATGCTAATAAATTGCTCAAAAATG 33 3127 CCGTTAAGTTTGCAGGATTTGACAGGTCTGGAACACATGCTAATAATTGCTCAAAATG 31	3345 CTICCTGCTGATATCAGGGGCTAATATATTCCACCAACTCAGGAATCCTACTATGAT 34  [	3405 CCCAACCIGCCACCGGTCACTAAAACTCTAGTAACAAACTGTAAACTGGTAACTGGAAAA 34 [	3465 ATCCACAAACCATATAAGACAAAAACAAATATAGGTTTGAAATCATGGGAAAACAAAAA 35	3525 ATCGCTTTTAAAATCATTCCTACCACCTTTCTCATCGGTTGCCACTTGGAT  3367 ATCGCTTTTAAAATGATTCGTACCAACGTTTCTCATGTGGGTTGGCCAGTTGGAT	3427 AGAAADAACCCTAGGAAGTTTGTTTGCCTGAATGACACACACACAC	3487 GCTCACACTCAAGGCTGTTCTCACGGACTTCTATGAATCCATGTTCCCCATACCTTCC 33	3705 CAATTGAACTGCCAAGAGATTTCGAAACCGTTTCCTTCATAGCAGGACTGCAGGAGAGTAGAGAA 3/ [	3765 TGGAGGGCTTATCGACAAATTGAAGTTTTGGACCCATTGTGTACAGCAACAATTGAT 3607 TGGAGGGCTTATCGAGACAAATTGAAGTTTTGGACCCATTGTGTACTAGCAACATTGTTTTTTTGAACCCATTGTGTACTAGCAACATTGTTTTTTTT	OY 3828 ATCTITACTATATTCTCATTTTTGCTCAGCASTAATTGCACTTAACCGGAAGATT 383  DD 3667 ATCTITACTATATTCTCATTTTTGCTCAGCAGTTAATTGCACTTAAGCGGAAGATATT 372
1507 AGIGICICTIACIGIAATCAGGGATGIGCGAATTCCTGGCTCGCTGGTAAGTTCTGTGAC 1568 1725 CAAGCATGCTATGTCCTGTGGGTTTGATGCTGGCGACTGTGGGCAAGATCATTT 1784 1567 CAAGCATGCAATGTTGTCCTGTGGGTTTGATGCTGGGGACTGTGGGCAAGATCATTT 1626	CATGAATIGTATAAGTGATCCTTCTCCCAAACCAGACTACTATTATTACA 	1845 GAATGCCTGCCTTATTTCAGCTTTGCAGAAGTAGCCAAAAGAGGAGTTGAAGGTGCCTAT 1904 	AGTGACAATCCAATAATTCGACATGCTTCTATTGCCAACAAGTGGAAAACCA 	1965 ATAATGCACAGTGGAATGCCACCACAATACATTTTAATCTCACGTTTCAAAATACA 2024 	ARCGATGAAGAGTTCAAAATGCAGATAACAGTGGAGGGACACAAGGGAAG 	CTGAATTCTACGGCCCAGAAGGGTTACGAAAATTTAGTTAG	GAGGGGAAATCTTTTGAGGATATTCCCAAAGAAAAGGCTTCCGAAGTTTAAGAG 22	CATCHIGITAACTCAACAAGAAGACCCAGGAAGAGAGAAATTCCCCTGGTAATTT Z	TCACTCCTTCCAAAAGACGCCCAGTTGAGTCTCAATACCTTGGAITTGCAA 	GGGGGACATCACTTTGAAAGGATACAATTTGTCCAAGTCAGCCTTGCTGAGA 	atgaactcacagcatgctaaaataaaaatcaagctataataacagatgaaa 	2445 AGITIGGIGGCICCACAGGAAAACAGGIICATAAAAGCAICITGCCAAACAGCIITAGGA 2504 	2505 GTGTCTGAAAGATTGCAGAGGTTGACTTTTCCTGCAGTGTATAAAGTGAAAGGCTCAT 2564 	2565 GACCAGGGTCAGAATCCACCCCTGGACTTGGAGACCAGCAGCAGATTTAGAGTGGAAACT 2624	2625 CACACCCAAAAAACCATAGGCGGAAATGTGACAAAAGAAAG	2685 CCACTGGAAAGCCAGATGACAAAAGAAAAATCACAGGGAAAGAAA	2745 AGAATGGAGAAAATGCTGAAAATCACATAGGGTTACTGAAGTGTTACTTGGAAGAAG 2804 

295 477 8 6 8 6 6 6 6 6 6 6 6 6 6 음 중 음 8 6 ò 셤 ò 셤 상 점 8 8 8 95 PP ò 8 8 8 ô ∢ 356 416 Novel N-acetylglucosamine-1-phosphotransferase and N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase, useful for producing phosphorylated lysosomal hydrolase for treating lysosomal storage 174 234 The invention relates to a novel isolated human N-acetylglucosamine-1phosphotranaferase (GlorAc-phosphotraneferase) (I) and phosphodiester
alpha-GLCNAGASE (N-acetylglucosamine-1-phosphodiester alpha-NAcetylglucosaminidase) (II). The protein of the invention has
nephrotropic activity, and may be useful in enzyme replacement therapy. A
phosphorylated lysosomal hydrolase. The phosphorylated hydrolase
phosphorylated lysosomal hydrolase. The phosphorylated hydrolase
comprising a terminal mannose-6-phosphate, is useful for treating a
patient suffering from a lysosomal storage disease. The present sequence
is used in the exemplification of the invention CCCAGAAGGAGGATACACAAAGAAGCTAGTCCCAATCGAATCAGAGTATAGAAGATC 3941 3783 AGCCGAGATCAATACCATGTTTTGTTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCC TITCAGAATCGGCTITGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGC Gaps Human; N-acetylglucosamine-1-phosphotransferase; nephrotropic; GlcNAc-phosphotranferase; phosphodiester alpha-GlcNAcase; N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase; enzyme replacement therapy; phosphorylated lysosomal hydrolase; lysosomal storage disease; gene; ss. CCCAGAAGGAGGATACACAAAGAAGCTAGTCCCAATCGAATCAGAGTATAGAAGATC DB 4; Length 3621; ., Sequence 3621 BP; 1156 A; 743 C; 802 G; 920 T; 0 U; 0 Other; Indels GlcNAc-phosphotransferase related cDNA SEQ ID NO: 11; Similarity 99.7%; Pred. No. 0; 22; Conservative 0; Mismatches (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC. Example 10; Page 54-55; 62pp; English standard; cDNA; 3621 99US-0153831P. (first entry) WPI; 2001-290356/30. 10-AUG-2000; US6537785-B1 14-SEP-1999; X. Best Local Simi Matches 3492; 01-AUG-2003 25-MAR-2003 3885 3727 115 357 175 297 ACC81011 ACC81011 Canfield diseases Query Match Human Homo RESULT

1016 1076 1136 1196 1074 1436 896 926 959 836 654 714 774 894 414 474 716 534 776 594 CAGACAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATG CAGTTAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTCCTGGACCCAGCC TTTGACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGA CAGACACTATGGAGGGGCTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATG CAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAGGAAACAAATCAACTAAAA ACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC AGTGTAGCGCTTCTAAAACTGAATAACCCCAAGGATTTTCAAGAATTGAATAAGCAAACT AAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTATTGG GATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAGAGGCATGCACCATGGGTTCGG CTAAATGATGATGATCATGTTTGGGGAAGGATGTCTGGCCCAGATGATTTTTACAGTCACTCC CAGITAGAGIGITIGCIAACACACIGCATIAAGGIGCCAAIGCIIGIACIGGACCCAGCC AGTGACATTTTCAATGTTGCAAAAACCAAAAACCCTTCTACCAATGTCTCAGTTGTT CAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAGGAAACAAATCAACTAAAA ACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC AGTGTAGCGCTTCTAAAAACTGAATAACCCCAAGGATTTTCAAGAATTGAATAAGCAAACT AAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATGG GATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTTGAA GATCTGAGGGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAA GATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAGAGGCATGCACCATGGGTTCGG Greacaaragracacaccaccaccargrirricgaaarricaagccacrigccraccriragr CTAAATGATGATGTCATGTTTGGGAAGGATGTCTGGCCAGATGATTTTTACAGTCACTCC AGTGACATITICAAIGITGCAAAACCAAAAACCCTICTACCAAIGICICAGIIGIT TITGACAGIACIAAGGAIGIIGAAGAIGCCCACICTGGACIGCIIAAAGGAAAIAGCAGA AATATTTTCATTGTCACCAACGGGAGATTCCATCCTGGCTGAACCTTGACAATCCTCGA GTGACAATAGTAACACACCAGGATGTTTTTCGAAATTTTGAGCCACTTGCCTACCTTTAGT AAAGGCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAGGGCTGCCCAGGT TCCTGGATTAAGGATGGCTATTGTGACAAGGCTTGTAATAATTCAGCCTGCGATTGGGAT GGTGGGGATTGCTCTGGAAACAGTGGAGGGGGTCGCTATATTGCAGGAGGTGGAGGTACT 1557 1017 1077 1137 1197 1015 1257 1075 1317 1135 1377 1195 1437 1255 1497 1315 537 355 415 475 717 535 777 595 655 897 715 957 775 835 895 955 597 657 837 DP DP

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. 0		a &	2515 CAGATGACAAAAGAAAAGAAATCACAGGAAAAGAAAAAAGAACAACATAGAATGGAGTAA 2574 2757 AATGCTGAAAATCACATAGGCGTTACTGAAGTGTTACTTGGAAGAAAGGAAGG
<b>&gt;</b> 0	1677 TGTAATCAGGGATGTGCGAATTCCTGGCTCGCTGATAAGTTCTGTGACCAAGCATGCAAT 1736 	qa d	AATGCTGAAAATCACATAGGCGTTACTGAAGTGTTACTTGGAAGAAAGCTGCAGCATTAC 263
<b>5</b> 0	1737 GTCTTGTCCTGTGGGGTTTGATGCTGGGGCAAGATCATTTTCATGAATTGTAT 1796	o S	2817 ACAGATACTTACTTGGCTTTTTGCCATGGGAAAAAAAAGTTTTCCAGATCTTCTC 2876 
	AAAGTGATCCTTCTCCCAAACCAGACTCACTATATTATTCCAAAAGGTGAATGCCTGCC	ζ O	2877 GACGAAGAAGACTCATTGAAGACACAATTGGCATACTTCACTGATAGCAAAAATACTGGG 2936 
<b>~</b> 0	TATTICAGCITIGCAGAAGIAGCCAAAAGAGAGTIGAAGGIGCCIATAGIGACAAICCA TATTICAGCITIGCAGAGAGAGAGAGAGAGAGTICAAAGGGGCCTAAAGAGAAACAATCCA	yo d	2937 AGGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGTAAATATAAATTCTAAATAGC 2996 
	ATAATTCGACATGCTTCTATTGCCAACAAGTGGAAAACCATCCACCTCATAATGCACAGT	oy Oy	2997 AAGTITGGAITCACAICGCGGAAAGICCCTGCICACAIGCCTCACAIGAITGACCGGAIT 3056
n % (	ATAMILOGACAIGCIIITAIIGCCAACAAGIGGAAAAACCAICCAACIICAAAGAGGCAAGGAAGG	çy Op	3057 GTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGACAAGACGTCATTTCACAAA 3116 
n <b>&gt;</b> 1	GSAALGAATIGCCACCACAATACATTITAATCICACGTITCAAAATACAAAACGATGAAAGGGGTTTCAAAATACAAAACGATGAAATGAGGGTTCACGAAAAACAAAACAAAAAAAA	Qy	3117 GTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTTATTTTATTATTATCTCATGAGTGCA 3176 [
o <b>~</b>	TICAAAAIGCAGATAACAGTGGGAGGTGGGACAAAGGGGACCAAAACTGAATTCTACG GCCCAGAAGGGTTACGAAAATTTAGTTAGTTCCCATAACACTTCTTCCAGAGGCGGAAATC 	Qy Dp	3177 GTGCAGCCACTGAATATATCTCAAGTCTTTGATGAAGTTGATACAGATCAATCTGGTGTC 3236
0 ~	GCCCAGAAGGGTTACGAAAATTTAGTTAGTCCCATAACACTTCTTCCAGAGGGGGGAAATC CTTTTGAGGATATTCCCAAAGAAAAACGCTTCCCGAAGTTTAAGAGACATGATGTTAAC	6 6	3237 TIGICIGACAGAGAAATCCGAACACIGGCIACCGGAAITCACGAACIGCCGTIAAGITIG 3296 105 TIGICIGACAGAGAAATCCGAACACIGGCIACCAGAAITCACGAACIGCCGTIAAGITIG 3114
0 >	CTTTTTGAGGATATTCCCAAGAAAACGCTTCCCGAAGTTTAAGAGACATGATGTTAAC TCAACAAGGAGAGCCCAGGAAGAGGTGAAAATTCCCCTGGTAAATATTTCACTCCTTCCA 	S S	3297 CAGGAITTGACAGGTCTGGAACACATGCTAATAAATTGCTCAAAAATGCTTCCTGCTGAT 3356
0 ~	TCAACAAGGAGAGGCCCAGGAAGAGGTGAAAATTCCCCTGGTAAATATTTCACTCCTTCCA AAAGACGCCCAGTTGAGTCTCAATACCTTGGATTTGCAACTGGAACATGGAACATCACT	Qy Db	3357 ATCACGCAGCTAAATAATACTCCACCAACTCAGGAATCCTACTATGATCCCAACCTGCCA 3416
0 %	AAAGAUGCCCAGTIGAGTCTCAATACCTTGGAATTTGCAACTGGAACATGGAACATCACT TTGAAAGGATACAATTTGTCCAAGTCAGCCTTGCTGAGATCATTTCTGATGAACTCACAG	Qy	3417 CCGGTCACTAAAAGTCTAGTAACAAACTGTAAACCAGTAACTGACAAAATCCACAAAAGCA 3476
0 \$	TIGAAAGGAIACAATTIGICCAAGGCAGCCTIGCIGAGATCATTICIGAIGAACTCAGGCAGGCTAAAATAAATAAAAAAAAAA	ςς Op	3477 TATAAGGACAAAACAAATATAGGTTTGAAATCATGGGAGAAGAAATCGCTTTTAA 3536 
0 5	CATGCTAAAATSAAAAATCAAGCTATAATAACAGATGAAACAAATGACAGTTTGGTGGCT CCACAGGAAAAACAGGTTCATAAAAGCATCTTGCCAAACAGCTTTAGGAGTGTTCTGAAAGA	oy G	3537 AIGAITICGIACCAACGITICTCAIGIGGITIGGCCAGITIGGAIGACAIAAGAAAAACCCT 3596
0 5	CCACAGGAAAAACAGGIICAIAAAAGCAICTIGCCAAACACIITAGGAGIGICIGAAAGA  TIGCAGAGGGIIGACTITICCIGCAGIGAGIGIAAAAGIGAAIGGICAIGACCAGGGICAG	Oy Dp	3597 AGGAAGTTTGCCTGAATGACAACATTGACCACAATCATAAAGATGCTCAGACAGTG 3656 
0 >	2335 TTGCAGAGGTTGACTTTTCCTGCAGTGTGTAAAAGTGAATGGTCATGACCAGGGTCAG 2394 2577 AATCCACCCTGGACTTGGAGACCACAGCAAGATTTAGAGTGGAAACTCACACCCAAAAA 2636	λό dd	3657 AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCATACCTTCCCAATTTGAACTG 3716
0 \	2395 AATCCACCCTGGACTTGGAGACCACCAGCAGTTTAGAGTGGAAACTCACACCCAAAAA 2454 2637 ACCATAGGCGGAAATGTGACAAAAGAAAAGCCCCCATCTCTGATTGTTCCACTGGAAAGC 2696 	Qy Db	

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lysosomal storage disease e.g. Fabry's disease by contacting the protein
with a soluble GlcNAc-phosphotransferase and producing a phosphorylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing a high mannose glycoprotein for treating lysosomal storage disease, comprises culturing the lectin resistant mammalian cell in the presence of deoxymannojirimycin and kifunensine.
                                                                                                                                                                                                                                                                       Mannose glycoprotein; gene therapy; carbohydrate deficient cell; lysosomal storage disease; N-acetylglucosamine-1-phosphotransferase; gastrointestinal; gene; ds; lectin resistant cell; deoxymannojirimycin; kifunensine; glycosylation inhibition.
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phosphotransferase"
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Best Local Similarity 99.5%;
Matches 3477; Conservative
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                  TTTCAGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTTTACACCTGGGTGAATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a method of producing a glycoprotein having reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is N-acetylglucosamine (GlCNAc)-
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 <u> AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCCATACCTTCCCCAATTTGAACTG</u>
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                                                                     CCAAGAGAGTATCGAAACCGTTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGCTTAT
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                                                    CCAAGAGAGTATCGAAACCGTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGCTTAT
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                                                                                                                                                                                                                                                                                                          Glycoprotein, lectin, lysosomal storage disease, gastrointestinal, N-acetylglucosamine-1-phosphotransferase, gene, gene therapy, ss.
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1. .3600
7.4rag= a
/product= "N-acetylglucosamine-1(GlCNAc)
phosphotransferase"
                                                                                                                                                                                                                                                                                 N-acetylglucosamine-1(GlcNAc)-phosphotransferase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 8-10; 46pp; English
                                                                                                                                                                                                    BP.
                                                                                                                                  3598
                                                                                                       CGAGACAAATTGAAGT 3792
                                                                                                                                                                                                    standard; cDNA; 3600
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illarity 99.5%;
Conservative 0
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                                                                                                                          CGAGACAAATTGAAGT
                                                                                                                                                                                                                                                       (first entry)
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P-PSDB; ABW01536.
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3477; Conserv
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                                                                                                                                                                                                                                                                                                                                                  Unidentified
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AGGAAGTTTGTTTGCCTGAATGACAATGACCACAAATCATAAAGATGCTCAGACAGTG 3462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel N-acetylglucosamine-1-phosphotransferase and N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase, useful for producing phosphorylated lysosomal hydrolase for treating lysosomal storage diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated human N-acetylglucosamine-1-phosphotransferase (GlcNAc-phosphotranferase) (I) and phosphodiester alpha-GlcNAcase (N-acetylglucosamine-1-phosphodiester alpha-N-Actylglucosaminidase) (II). The protein of the invention has nephrotropic activity, and may be useful in enzyme replacement therapy. A protein of the invention (I), (II) is useful for preparing a protein of the invention (I), (II) is useful for preparing a phosphorylated lysosomal hydrolase. The phosphorylated hydrolase comprising a terminal mannose-6-phosphate, is useful for treating a patient suffering from a lysosomal storage disease. The present sequence is used in the exemplification of the invention
                                                                         CCAAGAGAGTATCGAAACCGTTTCCTTCATATGCATGCAGGAGGGATATGGAGGGCTTTC
                                 CCAAGAGAGTATCGAAACCGTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGGCTTAT
                                                                                                                                                                                                                                                                     Mouse; N-acetylglucosamine-1-phosphotransferase; nephrotropic; GlCNAc-phosphotranferase; phosphodiester alpha-GlCNAcase; gene; ss; N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase; enzyme replacement therapy; phosphorylated lysosomal hydrolase; lysosomal storage disease; enzyme; beta-subunit; alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5229 BP; 1485 A; 1242 C; 1199 G; 1302 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.4%; Score 2820.8; DB 4; Length 5229; llarity 79.1%; Pred. No. 0; Conservative 1; Mismatches 833; Indels 137;
                                                                                                                                                                                                                                                Murine GlcNAc-phosphotransferase alpha/beta-subunit cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47-49; 62pp; English.
                                                                                                                                                                                    B
                                                                                                                      CGAGACAATTGAAGT 3792
                                                                                                                                                                                  standard; cDNA; 5229
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0153831P.
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P-PSDB; ABR61380, ABR61384.
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CACAGGTATGGGCTCTACGTGCTTCTTGGGCGTCGTTGTCACCATCGTCTCCGCCTTC
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CGTGGAAATGTACATA--CAGACAAAAGTGCCTCACTTCAGAAATGAGTAGTGCTGATGG

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The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble GlcNAc-phosphotransferase (UDP-N-acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease. The present sequence represents a GlcNAc-phosphotransferase associated DNA. Phosphorylating a protein for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease by contacting the protein with a soluble GloNac-phosphotransferase and producing a phosphorylated protein. 9 ds, mouse; protein phosphorylation; soluble GlcNAc-phosphotransferase; UDP-N-acetylglucosamine; lysosomal storage disease; Fabry's disease; Gaps DB 10; Length 5229; Sequence 5229 BP; 1485 A; 1242 C; 1199 G; 1302 T; 0 U; 1 Other; 833; Indels 137; Similarity 79.1%; Pred. No. 0; 77. Conservative 1; Mismatches GlcNAc-phosphotransferase associated DNA Disclosure; SEQ ID NO 8; 55pp; English. BP. ADD27816 standard; DNA; 5229 2001US-00023888 21-DEC-2001; 2001US-00023888 (NOVA-) NOVAZYME PHARM INC. entry) (first Kudo M; WPI; 2003-801323/75. US2003119088-A1 21-DEC-2001; Mus musculus Canfield W, 15-JAN-2004 26-JUN-2003. Best Local Simi Matches 3667; ADD27816, Match RESULT 13 ADD27816

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       CATCTGAAATGCTTTGTAATTATTGACTTCAGCCCCTAAGAATGCTATGATTTCACGTGC
                                              cerrgaaagrecrrerrraacrcarreccaagaaracrereacre
                                                                                                                                          4397 GGGCCTGATTGCGAAGGGCTAGTGTCACGTAGCAGTGCTGCTCACCGGATGTAATTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse cDNA #1 used to illustrate the method of the invention
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illustrate the method of the invention
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දු ද	1467 GTGCCAAACTGTGCCGAGGGCTGCCCAGGTTCCTGGATTAAGGATGCTATTGTGACAAG 1526 	g qq	2392 GTGACCGTGAAGGCCGTGACCACGCTTTGAATCCACCCCGGGT
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8 & 8	AGTCGCTATATTGCAGGAGGTGGAGGTACTGGGAGTATTGGAGTTGGACACCCCTGGCAG	Qy QD	2667 CCCCCATCTCTGATTGTTCCACTGGAAAGCCAGATGACAAAAGA 2497 CTTTCACCGCTGATCGTTCCCCCCAGAAAGCCACTTGCCAAAAGA
3 6 6		ò q	2727 AAAGAAAAGAGAACAGTAGAATGGAGGAAAATGCTGAAAATCA 
3 & 1	SCIGATAAGITICIGIAAGAAGCAIGCAAIGCAAIGTCITGICCAGGGTTIGAAGCTGGCGAC 1	Qy Dp	2787 GIGTIACTIGGAAGAAGCIGCAGCAITACACAGAIAGITACIT. 2587 ITAGIGCCIGGCAGACGGIIGCAGCAGAAITAICC
3 & 4		S S	2847 GAGAAAAAAGTATTTCCAAGATCTTCTCGACGAAGAAGAGTC.
3 & A		کی <sub>.</sub> و	2907 GCATACTTCACTGATAGCAAAATACTGGGAGGGAACTAAAAGA' 2698 GCGTACTTTACAGACCGCAAACATACCGGGAGGCAACTAAAAGA'
8 8	GGAGTTGAAGGTGCCTATAGTGACAATCCAATAATTCGACATGCTTCTATTGCCAACAAGAAGTTGAAGAACTAAGGAACAAGGAACAACCCCATCATCGACAAGAACAAGGAACAAGGGAACAACCCATCGAACAAGGAACAACCCCATCGACAAGAAGAAGAACAAGAAGAAAGA	රු සි	2967 CTCAGATATGTAAATAAAATTCTAAATAGCAAGTTTGGATTCAC. 
3 6 8	TGGAAAACCATCCACCTCATAATGCACAGTGGAATGAATG	Š å	3027 GCTCACATGCCTCACATGATTGACCGGATTGTTATGCAAGAACTV
ે દે	CTCACGTTTCAAAATACAAACGATGAAGAGTTCAAAATGCAGATAACAGTGGAGGTGGACTTCAAAATGCAGATAACAGTGGAGGTGGACTTCAAAATGCAGATAACAGAGTGGAGTGGACTTCAACAACAGAAGAAGATTCAAAAAATCCAGATAAGAGATTGAAAAATCCAAAAAAATCCAAAAAAATCAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	රු යි	3087 GAAGAATTTGACAAGACGTCATTTCACAAAGTGCGCCATTCTGA 
8 & 8	ACAGGGGGGCCCAAAACTGAATTCTACGGCCCACAAGGGTTACGAAATTTAGTTAG	λό da	
<u>ک</u> ج	2127 CCCATAACACTICTICCAGAGGGGAAATCCTITITGAGGATATICCCAAAGAAAAAGG 2186	yo da	3207 GHTGAAGTIGATACAGATCAAICTGGTGTCTIGTCTGACAGAGA [
3 8 7	TTCCCGAAGTTTAAGAGACATGATGTTAACTCAACAAGAGAGCCCAGGAAAGAGGTGAAA	Qy	3267 ACCAGAATTCACGAACTGCCGTTAAGTTTGCAGGATTTGACAGG 3058 ACGAGAATTCACGACCTACCTTTAAGCTTGCAGGATTTGACAGG
8 & 8	TICCCCCAAGAICAGGAACACTGTAAAIGCAACAGGGAAATITCCAAGAAGGIGAAAAATTCCCCTTCCAACATGAAAAAAAAAA	<i>\$</i> €	3327 ATAATIGCICAAAATGCTTCCTGCTGATATCACGCGGGTAAA
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CTTTTCCTGCAGTGAGT 2546 || || || || || CTGCCCAGCAGAGAGA 2391 SABATCCGAACACTGGCT 3266 GETCTGGAACACATGCTA 3326 AGGITCATAAAAGCAIC 2486 CTTCTCACAGACG---- 2333 ATGTGACAAAGAAAG 2666 SAAAAGAAATCACAGGG 2726 2556 ACATAGGCGTTACTGAA 2786 CTGTACCTGTAAAGGAG 2586 TGGGCTTTTTGCCATGG 2846 CATTGAAGACACAATTG 2906 CATCGCGGAAGTCCCT 3026 TIGCAAGATATGTTCCCT 3086 SAGGATATGCAGTTTGCC 3146 AATAATATTCCACCAACT 3386 AGTCTAGTAACAAACTGT 3446 ACTIGAGACCACAGCA 2606 

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                                                                                                                                               GGTCAGTTGGATGACATCAGAAAAACCCCAGGAAGTTCGTTTGTCTGAATGACAACATT
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21; 209 The present invention provides a method of producing a glycoprotein having reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is mouse DNA used to illustrate the method Producing a glycoprotein with reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein for Gaps Length 5229; 1485 A; 1242 C; 1199 G; 1302 T; 0 U; 1 Other; 833; Indels 137; DB 10; Score 2820.8; Pred. No. 0; 1; Mismatches

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13.4   ACCOURTEGACGATTCATTCATANAGAGATTCATACTCATANAGAGATTCATCACCOCCUTANAGAGATTCATCACCOCCUTANAGAGATTCATCACCOCCUTANAGAGAGATTCATCACCOCCUTANAGAGAGATTCACCOCCUTANAGAGAGATTCACCOCCUTANAGAGAGATTCACCACACACACACACACACACACACACACA
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2221 CTGCTAAGGTCTTTCCTGGGGAATTCACTAAATACTAAATAAA

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RESULT 1

US-09-635-872A-4

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Sequence 4, Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE-
TITLE OF LINGENISCATION NUMBER: US/09/635,872A

CURRENT PELICATION NUMBER: US/09/635,872A

CURRENT PELICATION NUMBER: 60,153,831

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 5597
Sequence 12, Appl
Sequence 13, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 38, Appl
Sequence 38, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
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US-09-491-356C-1
US-09-491-356C-1
US-09-496-147-2
US-09-497-855A-38
US-09-497-855A-38
US-10-071-411A-2
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US-10-071-411A-2
US-09-539-333D-1
US-09-539-333D-1
US-09-539-333D-1
US-09-513-999C-18965
US-09-513-999C-14742
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ö GGCTCGCTGAGGCGCGGCGGCGGC 120 TATGGGCTCTACGTGCTTCTTGG 240 ACCAATGTCTCAGTTGTTGTTTTG 720 GAAGGGGTGATGCTGTTCAAGCTCC 180 STITACACCIGGGGAAAIGGCACAG 420 CCTACTAAGAAGAGTGAGAAGCAGT 540 ATGUTTGTACTGGACCCAGCCCTGC 600 PATCCTTCTTTCATTCTGCCAGTG 660 STCCCTGGATTAGTGCTAATGCAAG 840 TTGCAGTTGTATTCAGAGGCCAGTG 960 SAAGGGTGATGCTGTTCAAGCTCC 180 CTGCTTAAAGGAAATAGCAGACAGA 780 AGGAAACAATCAACTAAAACAA 900 SAACAGATGGAGGAGGAGGAAAG 480 TGAGCGCCCCGGAGGCTGTGACC 60 0; Indels 0; Gaps B 4; Length 5597;

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4001   CTCAGTTGGTTTTTGATAGACCAGACCTAGCAACTTTGTTTG	RESULT 4 US-09-986-552-4 US-09-986-552-4  Sequence 4, Application US/09986552  Patent No. 6670165  APPLICANT: CANFIELD, William APPLICANT: CANFIELD, William TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDRC TILE REFERENCE: 2150890377DIV CURRENT APPLICATION NUMBER: US/09/986,552 CURRENT APPLICATION NUMBER: 09/635,872 PRIOR APPLICATION NUMBER: 60/113,831 PRIOR FILING DATE: 2000-08-10 PRIOR PILING DATE: 1999-09-14  NUMBER OF SEQ ID NOS: 52
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entin version 3.1  mo sapiens  100.0%; Score 5597;	Sest Local Similarity 100.0%; Pred. No. 0;  Matches 5597; Conservative 0; Mismatches 0; Indels 0; Gaps  1 CGGAGCCGAGCGGCGCCGCGCGCGCCAACCAATGAGCGGCCCGGAGGCTGTGACC 60  1 CGAGCCGAGCGGCTCCGTCGCCGAGCTGCAATGAGCGCCCCGGAGGCTGTGACC 60	61 TGCGCGCGGCGGCCCGACCGGGCCCCTGAATGGCGGCTCGCTGAGGCGGCGGCGGCGCGC 120	121 GGCGGCTCCAGGCTCCTCGGGGCGTGGCGGTGAAGGGGTGATGCTGTTCAAGCTC 180  121 GGCGGCTCAGGCTCCTCGGGGCGTGGCGTGAAGGGGTGATGCTGTTCAAGCTC 180  181 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTTACGTGTTCTTG 240	181 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGGTATGGGCTCTACGTGTGTTCTTGG 240 241 GCGTCGTTGTCACATCGTCTCCGCTTCCAGTTCGAGAGGTGTTCTGGAATGGAGC 300	241 GCGTCGTTGTCACCATCGTCTCCGCCTTCCGGAGAGGTGGTTCTGGAATGGAGCC 30 301 GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 36 301 GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 36 301 GAGATCAATACAATATTTTTTTTTTTTTTTTTTTTTTTT	AGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGGTCGATGCGCAGG 4	ATCITGAACTACTGAAGGAACTACAGGTCAGAGAACAGATGGAGGAGGAGGAGGAAAG 4	481 CANTGAGAGAANTCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAAGCAGT 540	541 TAGAGTGTTTGCTAACACACTGCATTAAGGTGCCAATGCTTGTACTGGACCGGGCCTGC 600	601 CAGCCAACATCACCTGAAGGACGTGCCATCTCTTATCCTTCTTTTCATTCTGCCAGTG 660 [	661 ACATTITCAAIGITGCAAAACCAAAAACCCTICTACCAAIGICTCAGTIGITGITTITG 720 661 ACATTITCAAIGITGCAAAAACCAAAAACCTICTACCAAIGITCTAAGTGTCTCAGTIGITGITTITG 720	ATGCCCACTCTGGACTGCTTAAAGGAAATAG	CAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATGCAAAGAAGTATGGAGGGGGTACTTAATGCAAAAGAAAG	841 ATTIGGCTITCCTGAGTGGATTICCACCAACAATCAAGGAAACAAATCAACTAAAAAAAA 900 	aattgccagaaaatctttcctctaaagtcaaactgttgcagttgtattcagaggccagtg

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 4681 TGGAAATGTACATATTCAAACAGAAGTGCCTCATTTTAGAAATGAGTAGTGCTGATGGCA 4740	; FILE REFERENCE: 10929-0001-77 ; CURRENT APPLICATION NUMBER: 08/09/636,596C ; CURRENT APPLICATION NUMBER: 60/153,831 ; PRIOR APPLICATION NUMBER: 60/153,831 ; PRIOR FILING DATE: 1999-09-14 ; NUMBER OF SEQ ID NOS: 52 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 4
4801 CTCAGTTTTTGATAGAACAGAGCCAGCAACTTTCTTTGTAAAAGGCTGGTTAGT 4860 	; LENGTH: 5597 ; CRGAN: DNA ; CRGAN: Homo sapiens US-09-636-596C-4
4861 AAATTATTGCAGGCCACCTGTGTCTTTGTCATACATTCTTCTTGTTTGT	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 5597; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 4921 TITITICAAACAACCCTCTAAAAATGTAAAACCATGTTTAGCTTGCAGCTGTACAAAA 4980 	Oy 1 CGGAGCCGAGCGGCGCCCCGGAGCTGCAATGAGCGGCCCCGGAGGCTGTGACC 60
 4981 ACTGCCCACCAGCCAGATGTGACCCTCAGGCCATCATTTGCCAATCACTGAGAATTATTT 5040 4981 ACTGCCCACCAGCAGATGTGACCCTCAGGCCATCACTTGCCAATCACTGAGAATTATTT 5040	Oy 61 TGCGCGCGGCGGCCCCAACCGGGGCCCCTGAATGCGGGCTCGCTGAGGCGGCGCGCGC
 5041 TIGITGITGITGITGITGITTITGAGACAGAGICICCCCTCTCTGITGCCCAGGCTGGAG 5100	Oy 121 GGCGGCTCAGGCTCCTCGGGGCGTGGCGTGAGGGGTGATGCTGTTCAAGCTCC 180
5101 TGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCAGTTCTGTC 5160 5101 TGCAGTGGCGCAATCTCAGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCAGTTCTGTC 5160	QY 181 TGCAGAGACAAACCTATACCTGCCCTGCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240
 5161 TCAGCCTTCTGAGTAGCTGGGAGCTACAGGTGCCACCACCACCCTGCTAATTTTTGTA 5220	OY 241 GCGTCGTTGTCACCATCGTCTCCGCCTTCGGAGAGGTGGTTCTCGGATGGAGCC 300
5221 TITITAGTAGAGAGGGTTCCACCATATTGGTCAGGCTTATCTTGAACTCCTGACCTC 5280 	QY 301 GAGATCAATACCATGTTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360
5281 AGGIGATCCACCTGCCTCTGCCTCCCAAAGTGCTGAGATTACAGGCATAAGCCAGTGCAC 5340	Qy 361 AGAATCGCCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG 420

1501 GGATTAMGGATGGCTATTOTALCALAGGCTTGTALTALTCAGCCTGCGATTGGGATGGTT 1560 1561 GGATTAMGGATGGCTATTGTALAGGCTTGTALTALTCAGCTGCGATTGGGATGGTT 1560 1561 GGATTTAMGGATGGCAACCCCTGGAAGGATTGGTTGAAGGATTGGAAGGATGGTT 1660 1561 GTATTGGAGTTGGAACCCCTGGAGGATTGGTTGAAGGAATTGGAAGGATGTTTATTGAAGGATTGGAAGGATGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGAAGGAATTGGAAGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAAGGAATTGGAA
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121 AGANTGGGCTTTGCTGCCATTGCCATTGACCTCGTTTATCACCTGGTGAATGGCCAATGACCACAAAC  422 ATTTGACCTTTGCTGCAAACTCCATTGACCATCACTCGAAACTGGAACGACGACGAAC  423 ATTTGACCTTTCTTAAACTCTTGGAAACTCACTCACTCAC

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Pred. No. 0;
0; Mismatches
                                                                              Query Match 67.2%;
Best Local Similarity 99.7%;
Matches 3767; Conservative
SEQ ID NO 20
LENGTH: 3783
TYPE: DNA
ORGANISM: Homo sapiens
                                          ; ORGANISM: Hom
US-09-635-872A-20
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Patent NO. 6534300
GENERAL INFORMATION:
FAPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
FILE REFERENCE: 195611050
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
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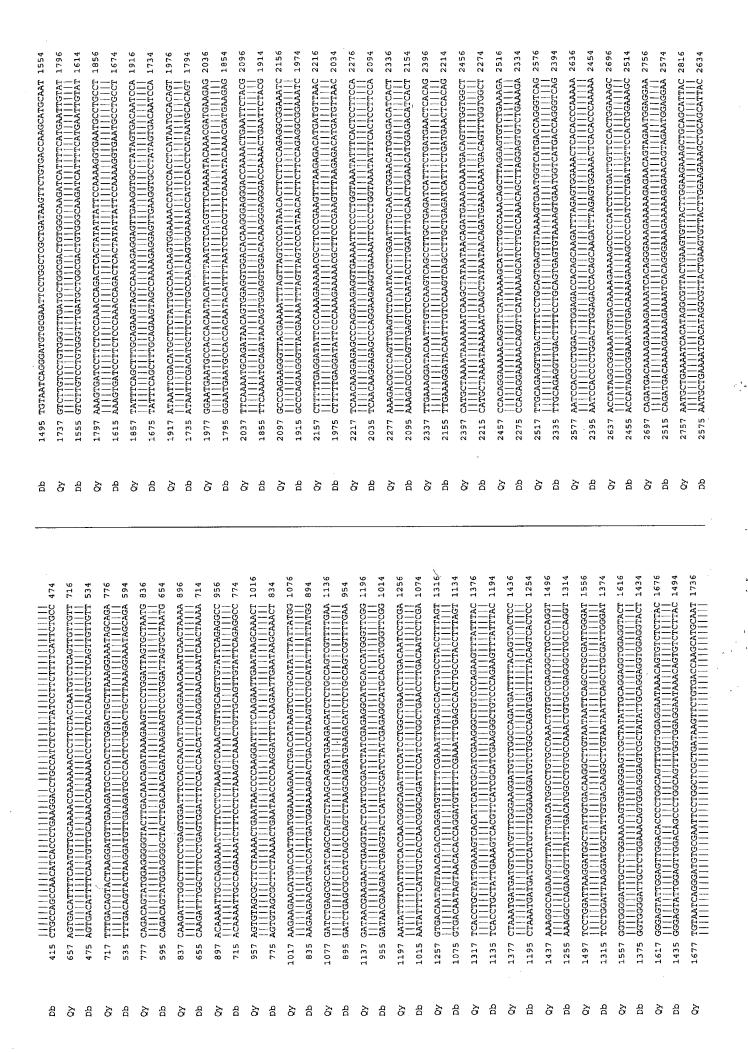
	AAGTCCTGCA	1065 TATTTATTATGGGATCTGAGGGCGATCAGGCGGTGAGGGGGGGG	1125 AGTCGTTTTGAAGATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAGAGGCATGCA 1184		1245 GACAATCCTCGAGTGACAATAGTAACACAGGATGTTTTTCGAAATTTGAGCCACTTG 1304  1087 GACAATCCTCGAGTGACAATAGTAACACAGGATGTTTTTCGAAATTTGAGCCACTTG 1304 1306 CATACATTGAGTGACAATAGTAACACAGGATGTTTTTCGAATTTGAGCCACTTG 1146	CCTACCTTTAGTTCACCTGCTATTGAAAGTCACGTTCATCGCATCGAAGGCTGTCCCAG	A AGITTATTTACCTAAATGATGATGTCATCTTTGGGAAGGATGTCTGGCCAGATGATTTTTTTT	FACAGTCACTCCAAAGGCCAGAAGGTTTATTGACAGGCCTGTGCCCAAGGCCTGTGCCGAGGCCTGTGCCGAGGCCTGTGCCGAGGCCTGTGCCGAGGCTTTATTTGACATGGCCTGTGCCCAAACTTGTTTGACATGGCCTGTGCCCAAACTGTGCCGAGGCCTGTGCCCAAACTGTCCGAGGCCTGTGCCCAAACTGTCCGAGGCCTGTGCCCAAACTGTCCGAGGCCTGTGCCCAAACTGCCCGAGGCCCTGTGCCCAAACTGCCCGAGGCCCTGTGCCGAAACTGCCCGAGAGCCTTTATTGACAAAAGGCTTGTGAAAAACTGCCAAACTGCCAAAACAAAAAAAA	GGCTGCCCAGGTTCCTGGATTAAGGATGGCTATTGTGACAAGGCTTCTAATAATTCAGCC 138 GGCTGCCCCAGGTTCCTGGATTAAGGATGGCTATTGTGACAAGGCTTCTAATAATTCAGCC 138	TGCGATTGGGATGGTGGGGATTGCTCTGGAAACAGTGGAGGGGAGTGGCTATATTGCAGGA 1	GGTGGAGGTACTGGGAGTATTGGAGTTGGACACCCTGGCAGTTTGGTGGAGGAATAAAC	n - 1		CALGARITGIATAAAAGIGATCCTTCTCCCAAACCAGACTACTATATTATTCCAAAAGGT C CANAMACCAMACTATATATATCCAAAAGGT C CANAMACCAMACTATATATATATATATATATATATATATATAT	GAATGCCTGCTTATTTCAGCTTTGCAGAAGTAGCCAAAAGAGGGGGTTGAAGGTGCCTATT	1905 AGTGACATOCATRATICGACATGCTICTATIGCCACCAGTGGAAACCATCATCATCT 1904
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RESULT 10 US-09-636-596C-20 S Sequence 20, Application US/09636596C Patent No. 6770468 GENERAL INFORMATION:	; APPLICANT: CANFIELD, WILLIAM ; TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNAcase OF THE LYSOSOMAL TARGETING PATHWAN ; TILE REPERENCE: 10929-0001-77 ; CURRENT APPLICATION NUMBER: US/09/636,596C ; CURRENT FILING DATE: 2000-08-10	PALOR APPLICATION UNDER: 1999-09-14; NUMBER OF SEQ ID NOS: 52; SOFTWARE: Patentin version 3.0; SOFTWARE: Patentin version 3.0	SEQ ID NO 20   LENGTH: 3783   TYPE: DNA   ORGANIZM: Homo sapiens	Obery Match  Query Match  Query Match  Best Local Similarity 99.7%; Pred. No. 0;  Matches 3767; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	CAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTC 22 	OY 225 TACGIGIGCTICTIGGGGGTCGTIGTCACCATCGTCTCCGCCTTCCAGITCGGAGGGG 284	OY 285 GITCIGGAAIGGAGCCGAGAIGAAIAACAIGTITIGIITGAITCCIAIAGAGACAAIAIT 344	Qy 345 GCTGGAAAGTCCTTTCAGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACC 404	OX 405 TGGGTGAATGGCACAGATCTTGAACTACTGAAGGAACTACAGCAGGTCAGAGAACAGATG 464	Qy 465 GAGGAGGAGAAAAGCAATGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAG 524	Oy 525 AAGAGTGAGAAGCAGTTAGAGTGTTTGCTAACACACTGCATTAAGGTGCCCAATGCTTGTA 584	OY 585 CTGGACCCAGCCCAGCCAACATCACCCTGAAGGACGTGCCATCTCTTATCCTTCT 644	Qy 645 THTCATHORCCAGHGACATHTHCAAHGTAGCCAAAAAACCCTHCTACCAAHGHC 704	Qy 705 TCAGTIGTITITGACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAA 764	OY 765 GGAAATAGCAGACAGACAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGA 824	Qy 825 TTAGTGCTAATGCAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTCAAGGAAACA 884 

AGTGTAGCGCTTCTAAAACTGAATAACCCCAAGGATTTCAAGAATTGAATAAGCAAACT 1016 ö AATATTTTCATTGTCACCAACGGCCAGATTCCATCCTGGCTGAACCTTGACAATCCTCGA CTGCCAGCCAACATCACCTGAAGGACGTGCCATCTTTTATCCTTTTCATTCTGCCCTGCCCACCAGCCAACATCGCGACCTGCCATCTTTATCCTTTTATCTTTTCTGCC CAGACAGTATGGAGGGGGTACTTGACAACAGATAAAGAAGTCCCTGGATTAGTGCTAATG GATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAA GATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCTCTGCCAGTCGTTTTGAA Gaps ., Length Indels DB 4; 11; Score 3485.4; Pred. No. 0; 0; Mismatches Query Match
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Db 3235 CCGGTCACTAAAAGTCTAGTAAACTGTAAACTGACAAAATCCACAAAGCA 3294  Oy 3477 TATAAGGACAAAAATATAGGTTTGAAATCATGGGAGAAGAAATCGCTTTTAAA 3536  Db 3295 TATAAGGACAAAAATATAGGTTTGAAATCATGGGAGAAGAAATCGCTTTTAAA 3554  Oy 3537 ATGATTCGTACCAACGTTTCTCATGTGGCAGAGGAAGAAATCCCTTTTTAAA 3554  Oy 3558 ATGATTCGTACCAACGTTTCTCATGTGGCAGAAGAAATACCTTTTTAAA 3554  Oy 3559 AGGAAGTTTGTTTGCTGAATGTTGGTTGGCCAGTTGGATGACTAAGAAAAACCT 3414  Oy 3557 AAGGATTTGTTTGCTGAATGACAACTTTGACCAAATAAAAAAACCT 3414  Oy 3557 AAGGATTTGTTTGCTGAATGACAACAATTCATAAAAATCTTAAAAAACCT 3414  Oy 3557 AAGGATTTGTTTGCTGAATGACAACTTTCACCAAATTGAATGATCAAGAAAAACCT 3414  Oy 3557 CCAAGAAGAATTTTTTTTTTTTTTAAAAATTCAATTAAAAATTCATTAAAAATTTGAATTTGAATTTGAATTTTTTTT	RESULT 12 US-09-636-077A-21 i Sequence 21, Application US/09636077A i Patent No. 6537785 i GENERAL INFORMATION; i APPLICANT: CANFIELD, WILLIAM i TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE i FILE REFERENCE: 195612USO i CURRENT FILING DATE: 2000-0810 i PRIOR PILING DATE: 1999-09-14 i NUMBER OF SEQ ID NOS: 52 i SOFFWARE: Patentin version 3.0 i SEQ ID NO 21 i LENGTH: 3621 i LENGTH: 3621 i LENGTH: 3621 i COSCANISM: Home sapiens US-09-636-077A-1	Query Match 62.3%; Score 3485.4; DB 4; Length 3621; Best Local Similarity 99.7%; Pred. No. 0; Matches 3492; Conservative 0; Mismatches 11; Indels 0; Gaps 0 Qy 297 AGCGGAGATCAATACCATGTTTTGTTTGAAGACAAAATTGCTGGAAAGTCC 356	Db 115 AGCCGAGATCAATACCATGTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCC 174  Qy 357 TITCAGAAATGGCCTTTGTCTGCCGATGCCGATTGACGTTGTTTACACCTGGGTGAATGGC 416	QY         417 ACAGAICTTGAAGGAACTACTGAAGGAACTACTGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	QY         477         AAAGCAATGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAAG         536           Db         295         AAAGCAATGAGAGAAATCCTTGGGAAAAACACAAACGGAACCTACTAAGAAGAGTGAGAAG         354	OY 537 CAGTIAGAGIGITIGCTAACACACTGCATTAAGGIGCCCAATGCTTGTACTGGACCCAGCC 596	Qy 597 CIGCCAGCCAACAICACCCIGAAGGACGIGCCAICTCTITAICCTICTTITCAITCIGCC 656
2337 TTGAAAGGATACAATTTGTCCAAGTCACCTTGCTGACATTTCTGATGAACTCACAG 2236 2155 TTGAAAGGATACAATTTGTCCAAGTCACCTTGCTGAATTTCTCGATGAACTCACAG 2214 2397 CATGCTAAAATAAAAAATTGTCCAAGTCATTATAACAGAATCAAACAATTTCTCGTGACT 2456 2215 CATGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2757 AATGCTGAAATCACATAGGCGTTACTGGAGGAGAAGCTGCAGCATTAC 2816 2575 AATGCTGAAATCACATAGGCGTTACTCGAAGTGTTACTTGGAAGAAGCTGCAGCATTAC 2816 2575 AATGCTGAAATCACATAGGCGTTACTCGAAGTGTTACTTGGAAGAACTGCAGCATTAC 2634 2817 ACAGATAGTTACTTGGGCTTTTTGCCATGGGAGAAAAAAGTATTTCCAAGATCTTCTC 2676 2635 ACAGATAGTTACTTGGGCTTTTTGCCATGGGAAAAAAAGTATTTCCTAGATCTTCTC 2694 2877 GACGAAGAAGACTCATTGAAGACACAATTGGCAAAAAAAA	3057 GTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGACAAGACGTCATTTCACAAA 3116	2935 GTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTCTTATTTTATTATCTCATGAGTGCA 2994 3177 GTGCAGCCACTGAATATATCTCAAGTCTTTGATGAAGTTGATACAGATCCATCGTGTC 3236 117 GTGCAGCCACTGAATATATCTCAAGTCTTTGATGAAGTTGATACAGATCAATCTGGTGTC 3054 2995 GTGCAGCACTGAATATGTCAAGTCTTTGATGAAGTTGATACAGATCAATCTGGTGTC 3054	3237 TTGTCTGACAGGAAAATCCGAACACTGGCTACCAGAATTCACGAACTGCCGTTAAGTTTG 3296 	3297 CAGGATTIGACAGGICTGGAACACAIGCTAATAAATTGCICAAAAATGCTTCCTGCTGAT 3356 	3357 ATCACGCAGCTAAATAATATTCCACCAACTCAGGAATCCTACTATGATCCCAACCTGCCA 3416 	3417 CCGGTCACTAAAAGTCTAGTAACAAACTGTAAACCAGTAACTGACAAAATCCACAAAGCA 3476



; Patent No. 6642038 ; GENERAL INFORMATION: ; APPLICANT: CANFIELD, WILLIAM M ; TITLE OF INVENTION: GLCNAC PHOSPHOTRANSFERASE OF THE LYSOSOMAL ; FILE REPREMENT: 2.101190180COMT ; CURRENT APPLICATION NUMBER: US/99/636,060C ; CURRENT FILING DATE: 2000-08-10 ; PRIOR APPLICATION NUMBER: 60/153,831 ; ROTHARE: PATENTION NUMBER: 60/153,831 ; ROTHARE: PATENTIN PATES: 1999-09-14 ; NUMBER OF SEQ ID NOS: 52 ; SOFTWARE: PATENTIN VERSION 3.1 ; SEQ ID NO 21 ; LENGTH: 3621 ; TYPE: DNA ; ORCANISM: Homo sapiens US-09-636-060C-21	Query Match 62.3%; Score 3485.4; DB 4 Best Local Similarity 99.7%; Pred. No. 0; Matches 3492; Conservative 0; Mismatches 11;	Oy 297 AGCCGAGATCAATACATGTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTC	OY 357 ITTCAGAAICGGCTITGICIGCCCAIGCCGAITGACGITGITTACACCIGGGGGGGGAGGCGCGGGGGGGGGG	OY 417 ACAGATCTTGAACTACTGAAGGAACTACAGGGGGTCAGAGAACAGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	OY 477 AAAGCAATGAGAAATCCTTGGGAAAAACACAACGGAACCTACTAAGAAGAGTGAGAAG	OY 537 CAGTTAGAGTGTTTGCTAACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCC	OY S97 CIGCCAGCCACATCACCCTGAAGGACGTGCCATCTTTATCCTTCTTTTCATTCTGCC	OY 657 AGRGACATTTCAARGITGCAAAACCAAAAAACCTTCTACCAATGICTCAGTTGTTGTT	OY 717 ITTGACAGTACTAAGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGA	OY 777 CAGACAGTAIGGAGGGGTACTIGACAACAGATAAGAAGTCCCTGGATTAGTGCTAATG	OY 837 CAAGATTTGGCTTTCCTGAGTGGATTTCCACCAACATTGAGGAAACAAATGAACTAAAA	QY 897 ACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC Db 715 ACAAAATTGCCAGAAATCTTTCCTCTAAAGTCAAAACTGTTGCAGTTGTATTCAGAGGCC	OY 957 AGTGTAGGCCTTCTAAAACTGAATAACCCCAAGGATTTGAAGAATTGAATAAGCAAACT
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RESULT 13 US-09-636-060C-21 ; Sequence 21, Application US/09636060C

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Db   3055   TTGTCTGACAGAGAAACCGAACCTGGCTACCAGAATTCACGAACTGCGGTTAAGTTTG   3114	RESULT 14  US-09-86-552-21  INSEQUENCE 21, Application US/09986552  Patent No. 6670165  GENERAL INFORMATION: PAPLICANT: CANTEINE William  ITILE REPRENCE: 120809807101V  CURRENT FILING DATE: 2010-11-09  PRIOR APPLICATION NUMBER: 00/15/918  PRIOR APPLICATION NUMBER: 00/15/918  PRIOR APPLICATION NUMBER: 00/15/911  PRIOR APPLICATION NUMBER: 00/15/91  PRIOR APPLICATION NU

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Oy         3717         CCAAGAGAGTATCGAAACGGTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGGCTTAT         377           Db         3535         CCAAGAGAGTATCGAAACGGTTTCCTTCATATGCATGAGCTGCAGGAATGGAGGCTTAT         359           Oy         3777         CCAGACAAATTGAAGTTTTGGAC         3799           Db         3595         CCAGAGACAAATTGAAGTAGTAGTC         3677	RESULT 15 US-09-636-596C-21 Sequence 21, Application US/09636596C Sequence 21, Application US/09636596C Sequence 21, Application US/09636596C Sequence 21, Application US/09636596C Sequence 21, Application Third Calfield Third Application US/09/09/09/09/09/09/09/09/09/09/09/09/09/	PRIOR FILING DATE: 1999-09-14 NUMBER OF SEQ ID NOS: 52 SOFTWARE: PatentIn version 3.0 SEQ ID NO 21 LENGTH: 3621 TYPE: DNA ORGANISM: Homo sapiens	Ouery Match 62.3%; Score 3485.4; DB 4; Length 3621; Best Local Similarity 99.7%; Pred. No. 0; Matches 3492; Conservative 0; Mismatches 11; Indels 0; Gaps 0 297 AGCCGAGATCAATACCATGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCC 356	17	ACAGATCTTGAACTACTGAACGAACTACACGATTGAACGTTGATTTACACCTGAGGAACAACGAACG	TGAGAAG 53         TGAGAAG 35	537 CAGTIAGAGTGTITGCIAACACACTGCAITAAGGTGCCAATGCTIGIACTGGACCCAGCC 596	597 CTGCCAGCCAACATCACCCTGAAGGACGTGCCATCTTTTATCCTTTTTCATTCTGCC 656 [	657 AGTGACATTITCAATGTTGCAAAACCAAAAACCCTTCTACCAATGTCTCAGTTGTTT 716	717 TITGACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGA 776	GCTAATG 8         GCTAATG 6	ACTAAAA 8         ACTAAAA 7

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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 25, Appli Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 26, Appl Sequence 10, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 402, Appl Sequence 402, Appl Sequence 402, Appl Sequence 402, Appl Sequence 42, Appl Sequence 42, Appl Sequence 42, Appl

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ALIGNMENTS

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Result Core Match Length DB ID Description

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yo da	4981 ACTGCCACCAGCAGATGTGACCCTCAGGCCATCATTTGCCAATCACTGAGAATTATTT 5040 4981 ACTGCCACCAGCAGATGTGACCCTCAGGCCATCATTTGCCAATCATCACTCAGAATTATTT 5040	Db 1 GGAGCCGAGCGGGCGTCGTCGCCGGAGCTGCATGAGCGGCGCCCGGAGGCTGAACC 60 Qy 61 TGCGCGGGGGCCCCCACCGGAGCCCCTGAATGGCGGCTCGCTGAGGCGGCGGCGGCGGCGC 120
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à a	5341   CCAGCCGAGAATTAGTATTTTATGTATGGTTAAACCTTGGCGTCTAGCCATATTTTATG 5400	Db 361 AGAATCGGCTTTGTCTGCCCATGCCGATTGTTTATACCTTGGATGGA
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ζς q <sub>Ω</sub>		Db 481 CANTGAGAAATCCTTGGGAAACACAGAACCTACTAAGAAGAGTGAGAGCAGT 540  Qy 541 TAGAGTGTTTGCTAACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCTGC 600
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RESULT 4 US-10-023-889-3 Sequence 3, Application US/10023889   Bublication No. US20030124652A1   GENERAL INPORMATION: APPLICANT: CANFIELD, William   TITLE OF INVENTION: DEFICIENT CELLS   TITLE OF INVENTION: DEFICIENT CELLS   FILE REFERENCE: 203512US77   CURRENT FILING DATE: 2001-12-21   NUMBER OF SEQ ID NOS: 21   SEQ ID NO 3   LENGTH: 5597   TYPRE: DATE: ACCORDANISM: HOW SET IN COMPLEX CARBONISES OF SEQ ID NOS: 21   SEQ ID NO 3   CORRANISM: Homo sapiens   US-10-023-889-3	Query Match         100.0%;         Score 5597;         DB 15;         Length 5597;           Best Local Similarity 100.0%;         Pred. No. 0;         0;         Indels 0;         Gaps 0;           QY         1 CGGAGCCGAGCGCTCCGTCGCGGAGCTGCAATGAGCGCCCCGGAGGCTGTGACC 60         0         0           Db         1 CGGAGCCGAGCGGCGTCCGTGCGGAGCTGCAATGAGCGGCGCCCGGAGGCTGTGACC 60         0           QY         61 TGGGCGCGGACCCGACCGGGGCCCTCGAATGAGCGGCGCGCGGGGGCGCGCGGGGCGCGCGGGCGCGCGGGG	12.1 GGCGGCTCCAGGCCTGGCGGGCGGTGAGGGTGATGCTGTTCAAGGTCC  18.1 TGCAGAGACAAACCTCTGGGGGCGTGGCGGTGAGGGTGATGCTGTTCAAGCTCC  18.1 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG  18.1 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG  24.1 GCGTCGTTGTCACATCCTTCCCACTTCCAGTTGGAGAATGGAATGGAATGGGCTTCTTGG  24.1 GCGTCGTTGTCACATCGTCTCCGCTTCCAGTTCGGAAATGGAATGGAATGGAATGGTCTTTGTTTG	

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; Sequence 3, Application US/10024197.
; Publication No US20030133924A1
; GENERAL INFORMATION:
; APPLICANT: CANFIELD, William
; TILLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETJ;
; TILLE OF INVENTION: HIGHLY PROSPHORYLATED ACID BETJ;
; TILLE OF INVENTION: TREATING GAUCHER'S DISEASE
; FILE REPRESENCE: 2097994US
; CURRENT APPLICATION NUMBER: US/10/024,197
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 3
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5597; Conservative 0; Mismatches
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; TYPE: DNA
; ORGANISM: Homo sapiens
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  CGTGCAGGTCTAATTTCAACAGGCTAGAGTTAGTACTACTTACCAGATGTAATTATGTTT
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; Publication No. US20030148460A1; GENERAL INFORMATION: ; APPLICANT: CANFIELD, WILLIAM ; TITLE OF INVENTION: PHOSHODIESTER ALPHA-GLCNAcase OF THE LYSOSOMAL TARGETING PATHWAY: ; FILE REFERENCE: 230397US77DIV ; CURRENT APPLICATION NUMBER: US/10/306,686	; CURRENT FILING DATE: 2002-11-29 ; PRIOR APPLICATION NUMBER: 09/636,596 ; PRIOR PILING DATE: 2000-08-10 ; PRIOR PADIJOTATION VIMPER: 60/153	PRIOR FILING DATE: 1999-08-14  NUMBER OF SEQ ID NOS: 52  SOFTWARE: Patentin version 3.1	; SEC 1D NO 3 4 ; LENCTH: 5597 ; TYPE: DNA 9 ; ORGANIZAR: Homo sapiens	Query Matc Best Local Matches 55	SCGGCGTCCGTCGCCGGAGCTGCAATGAGCGGCGCCCGGAGGCTGTGACC 60	61 TGCGCGCGCGCCCCGACCGGGGCCCCTGAATGGCGGCTGAAGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	TCAAGCTCC           FCAAGCTCC	OY 181 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240  Db 181 TGCAGAGACAAACCTATACCTGCCTGTCCCACAGGTATGGGCTCTACGTGTGCTTCTTGG 240	Qy         241         GCGTCGTTGTCACCATGGTCTCCGCTTCCAGTGCTGGTGGTTCTGGAATGGAGCC 300           Db         241         GCGTCGTTGTCACCATCGTCTCCGCTTCCGAGAGGTGGTTCTGGAATGGAGCC 300	QY 301 GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360  DD 301 GAGATCAATACCATGTTTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTC 360	Oy 361 AGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGAATGGCACAG 420	Qy 421 ATCTTGAACTACTGAAGGAACTACAGCTCAGAAACAGAGGAGGAGGAGCAGAAAG 480  Db 421 ATCTTGAACTACTGAAGGAACTACAGCAGGACCAGAAACAGATGGAGGAGGAGGAGCAGAAAG 480	Qy 481 CAATGAGAAAATCCTTGGGAAAAGCACAACGGAACCTACTAAGAAGGTGAGAGAGCAGT 540 Db 481 CAATGAGAGAAATCCTTGGGAAAACACAACGGAACCTAATAAGAAGAGTGAGAAGCGT 540	Oy 541 TAGAGTGTTTGCTAACACTGCATTAAGGTGCCAATGCTTGTACTGGACCCAGCCCTGC 600  Db 541 TAGAGTGTTTGCTAACACTGCATTAAGGTGCCAATGCTTGTACTGGACCAACCA	601 CAGCCAACATCACCCTGAAGACGTGCCATCTTTATATCCTTTTCATTCTGCCAGTG	Oy 661 ACATTITCAATOTIGCAAAACCAAAAAACCCTTCTACCAATGTCTCAGTIGTTGTTTTTG 720  Dh 661 ACATTITICAATGTTGCAAAAACAAAAAAACCTTCTACCAATGTCTCAGTTGTTTTTTTT	721 ACAGTACTAAGGATGTTGAAGATGCCCACTCTGGACTGCTTAAAGGAAATAGCAGACAGA

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i ò	TACAGTCACTCCAAAGGCCAGAAGGTTTATTTGACATGGCCTGTGCCAAACTGTGCCGAG 148	<i>ò</i> 8	2505 GTGTCTGAAAGATTGCAGAGGTTGACTTTTCCTGCAGTGAGTG
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yo da	2925 AAAAATACTGGGAGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGTAAATAAA	; GENERAL INFORMATION: ; APPLICANT: CANFIELD, WILLIAM M ; TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOWAL HYDROLASE:
ò a	2985 ATTCTAAATAGCAAGTTTGGATTCACATCGCGGAAAGTCCCTGCTCACATGCCTCACATG 3044	
λο 1	045 ATTGACCGGATTGTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGACAAGACG 3	; FRIOR FILING DATE: 1999-09-14; PRIOR FILING DATE: 1999-09-14; PRIOR APPLICATION NUMBER: US 09/635,872; PRIOR FILING DATE: 2000-08-10
qq	87 ATTGACCGGATTGTTATGCAAGAACTGCAAGATATGTTCCCTGAAGAATTTGA	; NUMBER OF SEQ ID NOS: 52 : SOFTWARE: PatentIn version 3.1
ර දු	3105 TCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTCTTATTTTTATTAT 3164 2947 TCATTTCACAAAGTGCGCCATTCTGGAATATGCAGTTTGCCTTCTTATTATTAT 306	; SEQ ID NO 21 ; LENGTH: 3621 ; TYPE: DA
λō	ın	; ORGANISM: Homo sapiens US-09-895-072-21
අଘ (	7 CTCATGAGTGCAGTGCAGCCACTGAATATATCTCAAGTCTTTGATGAAGTTGATACAGAT	Query Match 62.3%; Score 3485.4; DB 9; Length 3621; Best Local Similarity 99.7%; Pred. No. 0;
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Š t	3345 CTTCCTGCTGATATCACGCAGCTAAATATTTCCACCAACTCAGGAATCCTACTATGAT 3404	175 TTTCAGAATCGGCTTTGTCTGCCCATGCCGATTGACGTTGTTTACACCTGGGTGATGGC
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ð	'n	295 AAAGCAATGAGAGAAATCCTTGGGAAAAAGACAACGGAACCTACTAAGAAGAGTGAGAAG
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λō	885 CCCAGAAGGAGGATACACAAAGAAGCTAGTCCCCAATCGAATCAGAGTATAGAAGAT	Db 715 ACAAATTGCCAGAAAATTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC 774
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resour US-09- ; Sequ ; Pate	-895-072-21 uence 21, Application US/09895072 ent No. US20020025550A1	QY 1017 AAGAAGAACATGACCATTGATGGAAAAGAACTGACCATAAGTCCTGCATATTTATT

2157 CTTTTGAGGATATTCCCAAAGAAAACGCTTCCCGAAGTTTAAGAGACATGATGTTAAC 221  1975 CTTTTTGAGGATATTCCCAAAGAAAACGCTTCCCGAAGTTTAAGAGACATGATGTTAAC 203  2217 TCAACAAGGAGACCCAAGGAAGAGGTGAAAATTCCCCTGGTAAATATTTCACTCCTTCCA 227  2217 TCAACAAGGAGACCCAAGAAGAGGTGAAAATTCCCCTGGTAAATATTTCACTCCTTCCA 209  2277 AAAGACGCCCAGTTGAGTCTCAATACCTTGGATTTGCAACAAGAAGACATCCCTTCCA 209  2277 AAAGACGCCCAGTTGAGTCTCAATACCTTGGATTTGCAACAAGAACATCCTTCCA 203  2277 AAAGACGCCCAGTTGAGTCTCAATACCTTGGATTTGCAACAAGAACATCCTT 233  2295 AAAGACGCCCAGTTGATCTCAATACCTTGGATTTGCAACAACAACACTCACT	2155 TIGAAAGGATACAATTGTCCAAGTCAGCTTGCTGAGATCATTTGTGATGAACTGAGGG 221.  2397 CATGCTAAAATAAAAATCAAGCTATAATAACAGATGAAACAAATGACAGTTTGGTGGCT 245.  2115 CATGCTAAAATAAAAATCAAGCTATAATAACAGATGAAACAAATGACAGTTTGGTGGCT 227.  2457 CCACAGGAAAAACAGGTTCATAAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGA 251.  2457 CCACAGGAAAAACAGGTTCATAAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGA 251.  2275 CCACAGGAAAAAACAGGTTCATAAAAAGCATCTTGCCAAACAGCTTAGGAGTGTCTGAAAGA 233.	2517 TTGCAGGGTTGACTTTTCCTGCAGTGAGTGTAAAGTGAATGACTGAC	2637 ACCATAGGCGGAAATGTGACAAAAGAAAAGCCCCCATCTGATTGTTCCACTGGAAAGC 269 [	2757 MATGCTGAAATCACHTACTCAAGTGTTACTTGGAAGAAGCTGCAGCATTAC 281 2575 AATGCTGAAATCACHTAIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2977 GACGAAGAAGAGTCATTGAAGACACAATTGGGATACTTCACTGATAGCAAAAATACTGGG 2931 2695 GACGAAGAAGAGCACTTTGAAGACACAATTGGCATACTTCACTGATAGCAAAATACTGGG 275- 2937 AGGCAACTAAAAGATACATTGCAGATTCCCTCAGATATGTAAATTATAAATAGC 299 2755 AGGCAACTAAAAGATACATTTGCAGATTCCCTCAGATATGTAAATAAA	2997 AAGTTTGGATTCACATGGGGAAGTCCCTGGTCACATGATTGACGGGATT 3056	3117 GRGGGCATTCRGAGANATGCAGTTTGCCTTCTTATTTATTATCTCATGAGTGCA 3176 2935 GTGGGCCATTCTGAGGATATGCCTTCTCTTATTTTTATTATCTCTTGAGTGCA 3176 3177 GTGCAGCCACTGAATATATCTCAGTTTGCTCTTCTTATTTTTTTT
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	λό da	897 ACAAAATTGCCAGAAAATCTTTCCTCTAAAGTCAAACTGTTGCAGTTGTATTCAGAGGCC 956 [
CGAGACAAATTGAAGTAGTAGTC	à	7 AGTGTAGCGCTTCTAAAACTGAATAACCCCAAGGATTTTCAAGAATTGAATAAGCAAACT
SULT 14 -10-306-686-21 Sequence 21, Application US/10306686 Publication No. US20030148460A1	a & a	775 AGIGIAGCGCITCIAAAACIGAAIAACCCCAAGGAITITCAAGAAITGAAIAAGCAAACI 834 1017 AAGAAGAACAIGACCAITGAIGGAAAAGAACIGACCAIAAGITCCGCAIAITTAITAITAIGG 1076 1017 AAGAAGAACAIGACCAITGAIGGAAAAGAACIGACCAIAAGITCCTGCAIAITIAITAITAIGG 894
ENBEAL INFORMATION: APPLICANT: CANPIBLD, WILLIAM TITLE OF INVENTION: PHOSHODIESTER ALPHA-GLCNACASE OF THE LYSOSOMAL TARGETING PATHWAY FILE REFERENCE: 2303970S77DIV	S S	1077 GATCTGAGCGCCATCAGCCAGTCTAAGCAGATGAAGACATCTCTGCCAGTCGTTTTGAA 1136
CURRENT APPLICATION NUMBER: US/10/306,686  CURRENT PILING DATE: 2002-11-29  PRIOR APPLICATION NUMBER: 09/636,596  PRIOR FILING DATE: 2000-09-10	& ସ	1137 GATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAGGGGGGCATGCACCATGGGTTCGG 1196
PRIOR APPLICATION NUMBER: 60/153,831 PRIOR FILING DATE: 1999-08-14 NUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin version 3.1	ço qa	1197 AATATTTCATTGTCACCAAGGGGAGATTCCATCCTGGCTGAACCTTGACAATCCTGGA 1256
SEQ ID NO 21 LENGTH: 3621 TYPE: DNA ORGANISM: Homo sapiens	QV Dp	1257 GIGACAATAGTAACACACCAGGAIGTITITCGAAATTIGAGCCACTIGCCTACCTITAGT 1316
3%; Score 3485.4; DB 15; Length 3621; 7%; Pred, No. 0;	\$ 6 6	1317 TCACCTGCTATTGAAAGTCACATTCATGCATCGAAGGCTGTCCCAGAAGTTTATTAC 1376
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QO	3403 AGGAAGTT		3462
ò	3657 AAGGCTG	AAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCCATACCTTCCCCAATTTGAACTG	3716
qq	3463 AAGGCTG	TTCCCAATTTGAACTG	3522
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ò	3777 CGAGACA	CGAGACAAATTGAAGT 3792	
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CD656815 AGENCOURT
BG199915 R8T19211
CN426090 17006000
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Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Directionally cloned using the following adaptors:
5. TCGACCACGCGTCG-3. and
5. GACTAGTTCTAGATCGCAGCGGCCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Eukaryota, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I. (Dases I to 334)

I. (Dases I to 334)

I. (Dases I to 334)

I. (Dayblished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM1357 row: n. column: 10

High quality sequence stop: 626.

Location/Qualifiers
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AGENCOURT_8304671 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6193737 5', mRNA sequence.
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12988.994 Million cell updates/sec
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                                  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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UI-H-ED1-RST20259 UI-H-DT1-BX095637

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                                             Length 934;
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RESULT 2

/organism="Homo sapiens"

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/clone lib="nH M MGZ 124"

/clone lib 1016 bp mRNA linear EST 20-FEB-2002 5. mRNA sequence. BM544697 7 312 61 ccarcercescerrecagricesagaesterrecagaicagaaregaecesagareaarace 120 372 GICTGCCCATGCCGATTGACGTTGTTACACCTGGGTGAATGGCACAGATCTTGAACTAC 432 492 241 TGAAGGAACTACAGCAGGTCAGAGAACAGATGGAGGAGGAGCAGAAAGCAATGAGAAAA 300 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 1016)
NIH-WGC http://mgc.noi.nih.gov/. The superior of the superior o 1 ceraracersecreteceaeastratesecretaestratesecretesesesersers CCATCGTCTCCGCCTTCCAGTTCGGAGGGTGGTTCTGGAATGGAGCCGAGATCAATACC ATGITTTGTTTGATTCCTATAGAGACAATATTGCTGGAAAGTCCTTTCAGAATCGGCTTT TCCTTGGGAAAAACACACAACGGAACCTACTAAGAAGAGTGAGAAGCAGTTAGAGTGTTTGC CCTATACCTGCCTGTCCCACAGGTATGGGCCTCTACGTGTGCTTCTTGGGCGTGGTTGTCA TGAAGGAACTACAGCAGGTCAGAGAACAGATGGAGGAGGAGCAGAAAGCAATGAGAGAAA Gaps 5 Query Match 14.8%; Score 829.6; DB 4; Length 1016; Best Local Similarity 97.6%; Pred. No. 6e-123; Matches 863; Conservative 0; Mismatches 19; Indels 2; Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue procurement: Invitrogen

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TIGITGITGITGITGITGITTITIGAGACAGAGICTCICTCTGITGCCCAGGCTGGAGTGC 5103
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1:867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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E. 1 (Bases I to 994)

NIH-MGC http://mgc.nci.nih.gov/.

Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gow

Plate: LLAM12270 row: d column: 04

High quality sequence stop: 676.
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Homo sapiens cDNA clone IMAGE:5553363
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AGENCOURT 6476164 NIH MGC_85
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/wol_type="mRNA"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
E. 1 (bases 1 to 981)
S. NIH-MGC http://mgc.nci.nih.gov/.
L. Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
High quality sequence stops: 575.
Location/Qualifiers
Location/Qualifiers
                                                                                                                                 981 bp mRNA linear EST 29-MAR-2002
-6821868 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5934740
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AGENCOURT 6821868 NIH_MGC
5', mRNA Sequence.
BQ053143 GI:19812483
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BM452210.1 GI:18501250
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CONA. Library Preparation: Life Technologies, Inc.
CDNA. Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: Libral2200 row: g column: 20
High quality sequence stop: 717.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1118)
361 TTCTATGAATCCATGTTCCCCATACCTTCCCAATTGAACTGCCAAGAGAGTATCGAAAC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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us-10-023-888-3.rst

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Full Supplementary Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 855)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bidg. 31 Rm10A07 Bethesda, MD 20892

Email: Ggapbs-r@mail.nih.gov

Tissue Procurement: Irene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan piao and Minoru KO

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC C

can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 884.

I Location/Qualifiers

I Location/Qualifiers
                                                                                                                                                                                               CD657400

855 bp mRNA linear EST 18-JUN-2003
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(Long) Homo sapiens cDNA clone IMAGE:30420087 5', mRNA sequence.
CD657400
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                                                                                                  CD657400.1 GI:31899587
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Homo sapiens
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VERSION
KEYWORDS
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AUTHORS
TITLE
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1. .1118
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Technologies."
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                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                           Indels 15;
                                                                                                                                                                                                                             Length 1118;
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Pred. No. 5.5e-119;
0; Mismatches 46;
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Best Local Similarity 93.6'
Matches 885; Conservative
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extraction, and separated from free linkers by Centricon-100 column. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase [Takara's with a primer Sall-S for 25 cycles. The products were purified by phenol/chloroform extraction and Centricon-100 column. The cDNAs were digested with Sall and NoIL maxymes and cloned into Sall/NoII site of pcMV-SPORT6 plasmid vector. The average insert size is about 3.6kb."
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                                                                                                                                                                                                                         GTGGAAACTCACACCAAAAACCATAGGCGGAAATGTGACAAAAGAAAAGCCCCCATCT
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                                                                                                                                                Score 794.8; DB 6;
Pred. No. 2.3e-117;
0; Mismatches 15;
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ilarity 98.1%;
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tes 810; Conserv
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BM450679 1061 bp mRNA linear BST 05-FEB-2002
AGENCOURT_6394543 NIH_MGC_67 Home sapiens cDNA clone IMAGE:5494379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORI6; Site_1: Not1;
/note_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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Pred. No. 1.1e-113;
0; Mismatches 27; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:5494379"
                                                                                          5', mRNA sequence.
BM450679
BM450679.1 GI:18499719
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al Similarity 95.9%;
826; Conservative
                                                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                361 GACAAAATCCACAAAGCATATAAGGACAAAAAAAAAATATAGGTTTGAAATCATGGGAGAA 420
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                                                                                                                                                                                                                                                    3159 TATTATCTCATGAGTGCAGTGCACTGCATATATCTCAAGTCTTTGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                   61 TATTATCTCATGAGTGCAGTGCAGTCACTGAATATATCTCAAGTCTTTGATGAAGTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GAACHGCCGHTAAGHTHGCAGGATHGACAGGTCHGGAACACATGCTAATAAATHGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAATGCTTCCTGATATCACGCAGCTAAATAATATTCCACCAACTCAGGAATCCTAC
                                                                                                                                                                                          1 AAGACGICATITICACAAAGIGCGCCATICIGAGGATAIGCAGITIGCCTICICITATITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3579 GACATAAGAAAAAACCCTAGGAAGTTTGTTTGCCTGAATGACAACATTGACCACAATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3639 AAAGATGCTCAGACAGTGAAGGCTGTTCTCAGGGACTTCTATGAATCCATGTTCCCATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3758 GCAGGAATGGAGGCCTTATCGAGACAAATTGAAGTTTTGGACCCATTGTGTACTAGCAAC
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                                                                                                              Gaps
                                                         Length 854;
                                                                                                           Indels
                                                       Score 770; DB 5; I
Pred. No. 2.2e-113;
0; Mismatches 5;
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                                                    13.8%;
                                                    Query Match
Best Local Similarity 99.0
Matches 806; Conservative
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Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homolal interiors, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

Lobases 1 to 854)

National Institutes of Health, Mammalian Gene Collection (MGC)

Longholished (1999)

Longholished (1999)

Longholished (1999)

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CONLECT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

High quality sequence stop: 624.
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| /organism="Homo sapiens" |
| /organism="Homo sapiens" |
| /organism="Homo sapiens" |
| /organism="Homo sapiens" |
| /organism="INAGE: 6147890" |
| /issue_type="melanotic melanoma" |
| /issue_type="melanotic melanoma" |
| /issue_type="melanotic melanoma" |
| /issue_type="melanotic melanoma" |
| /issue_type="melanoma" |
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AGENCOURT_7936624 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6147890 5', mRNA sequence.
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BU171738.1 GI:22685722
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                                                                                                                                                                                               ATGCACCATGGGTTCGGAATATTTTCATTGTCACCAACGGGCAGATTCCATCCTGGCTGA 1239
                                                                                                                                                                                                                                                                                                                                                                                        ATGATTTTTACAGTCAC--TCCAAAGGCCAGAAGGTTATTTGACATGGCC---TGTGCC 1471
                                                                                                                                                   564
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                                                                                                                                                                                                                       CTGCCAGTCGTTTTGAAGATAACGAAGAACTGAGGTACTCATTGCGATCTATCGAGGGC
                                                                                                                                                                                                                                                                                              ACCTTGACAATCCTCGAGTGACAATAGTAACACACCAGGATGTTTTCGAAATTTGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 CCCAGAAGIITAITIACCIAAAIGAIGAITGCCIGITIIGGGAAAGAIGIICIGGCCCAG
CTGCATATTTATTATGGGATCTGAGCGCCATCAGCCAGTCTAAGCAGGATGAAGACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1472 AAACTGTGCCGAGGGCTGCCC 1492
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// hotce="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sall;
// hotce="Vector: pCMV-Sport6; Site 1: Not1; Site 2: Sall;
This is a long-transcript enriched cDNA library (Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]) from WA01
cell line. Undifferentiated human ES cell line WA01/H1
was obtained from Wicell Research Institute, Inc.,
Madison, Wi, cultured according to their instructions, on MEF feeders: They formed round colonies with defined edges and were positive for alkaline phosphatase, SER-4, OCT3, OCT4, REXI UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FIT3, SSEA-1, TUBB3, NES, GAFA9, and EOWES. When confluent (10-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV
(Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIOl Reagent from Invitrogen. Protocol ref; Genome Res. 11: 1533-1558 (2001). [PMID:11544199]) Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5-p6ATAGTTCAAGATGGCACCCCCTTTTTTTTTTTTT-3] from 3.49 of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal-4.6 for 25 cycles. The products were purified by pained from free linkers by Centricon-100 column. The cDNAs were amplified by promer Sall/NotI site of pCMV-SPORTE plasmid vector. The average insert size is about 3.6kb."
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Bases I to 867)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Onpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Badg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Trene Ginis and Mahendra Rao, NIA

Tissue Procurement: Trene Ginis and Mahendra Rao, NIA

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Preparation: Yulan Piao and Minoru Ko

CDNA Library Preparation: Yulan Piao and distribution information

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC C

can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llll.gov

Plate: NDAM495 row: h column: 06

High quality sequence stop: 657.

Location/Qualifiers
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/cell line="MAOH"
/lab host="DBINOB (TI phage-resistant)"
/clone lib="NIA Human H1 Embryonic Stem Cell cDNA Library
(Long)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30419981"
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AGENCOURT 8104616 Lupski sympathetic_trunk Homo sapiens CDNA clone IMAGE:6193590 5', mRNA sequence.
BQ720582.
BQ720582.1 GI:21859479
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3336 TCAAAAATGCTTCCTGCTGATATCACGCAGCTAAATATATTCCACCAACTCAGGAATCC 3395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 CACGAACTGCCCGTTAGTTTGCAGGATTNGACANGTCTGGAACACATGCNTATAAATTTG 729
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crgarrerrecaeregaaageceagargacaaaagaaaaagaaaarreacagggaaagaaaaa 130
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(Dases 1 to 929)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACAAGACGTCATTTCACAAAGTGCGCCATTCTGAGGATATGCAGTTTGCCTTCTTAT
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                                                                                    GGAAGAAAGCTGCAGCATTACACAGATAGTTACTTGGGCTTTTTGCCATGGGAAAAAA
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Email: cgapbs-r@mail.nih.gov
Itsue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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| /db /ref="HT1080" |
| /db /ref="taxon:9606" |
| /db /ref="taxon:96
                                                                                                                                                                                                                                                                                                                                                                            4142
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mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 783)
                                                     601 GICCCAATCGAATCAGAGTATAGAAGATCTTCATTTGAAAACCATCTACCTCAGCATTA
                                                                                                                                                                      CTGAGTATTTTAAAAACTCAGCTTCACAGAGATGTCTTTGTGATGGNAATGCTTTAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                               rdaaacrdarriracririraaagaarrdgcrccrgggacrigrcarccrrrrraraa
                                                                                                                                CTGAGCATTTTAAAACTCAGCTTCACAGAGATGTCTTTGTGATGTGA----TGCTTAGCAG
                                                                                                                                                                                                                                                     TTTGGCCCGAAGAAAAAAAAAAAAAAAAAAAAAAAAAACC---ATGCTGTTTTGTGGCATGAATATAGC
               GTCCCAATCGAATCAGAGTATAGAAGATCTTCATTTGAAAACCATCTACCTCAGCATTTA
                                                                                                                                                                                                                                                                                                             CCACTGACTA-GGAATTATTTAACCAACCCACTGAAAACTTGTGT----GTCGAGCAGCTC
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Pred. No. 3.5e-109;
0; Mismatches 7;
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Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
11329013
Contact: Scott J. Cain
Athersys, Inc.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Lupski_sympathetic_trunk"
/clone_lib="Lupski_sympathetic_trunk"
/clone_loctor: pCMV-SPORTG (Life Technologies); Site_l:
/Not1: Site_2: Sal1; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
- TGGACGCAGGGGGGGGG 3' and
5' -TGGACGGGTGCGA' and
5' -GACTAGTTGTAGATGGGGGGGGCGCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAGTTAATTGCACTTAAGCGGAAGATATTTCCCAGAAGGAGGATACACAAAGAAGCTA 3912
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13597 row: h column: 07
High quality sequence stop: 693.
Location/Qualifiers
1. 929
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/do_xref="mRNA"
/clone="mRNA"
/clone="mRNAGE:6193590"
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Pred. No. 1.1e-109;
0; Mismatches 43; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                      Ltissue_type="sympathetic trunk"
dev_stage="adult, 16 yr"
lab_host="DH10B"
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Best Local Similarity 93.8%;
Matches 845; Conservative (
                                                                                                                                                                                                                                                                                                                                                                   sex="male"
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COMMENT Contact: Daniela S. Gerhard, Ph.D.  Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 RandoA07 Bethesda, MD 20892 Email: cgapbs-r@mail.nih.gov Tissue Procurement: Irene Ginis and Mahendra Rao, NIA Tissue Procurement: Irene Ginis and Mahendra Rao, NIA CDNA Library Preparation: Yulan Piao and Minoru Ko CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MG c an be found through the I.M.A.G.E. Consortium/LINL at: http://image.llni.gov Plate: NDAM498 row: p column: 01 High quality sequence stop: 629. FEBATURES I. 89 unce / Organism="Homo sapiens"	/mol_type="mRNA" /db_xref="taxon:960" /clone="InAGA" /clone="InAGA" /clone="InAGA" /clone="InAGA" /clone="Your   The propertion   /clone   The prope	Madison, Wi, cultured according to their instructions, on MEF Geders. They formed round colonies with defined edges and were positive for alkaline phosphatase, SSEA-4, OCT3, OCT4, REXI, UTF, TERT, SOX2, CX43 and CX45. They are negative for GATA2, GATA4, PDX1, NCAM, MSX1, FLT3, SSEA-1, TUBB3, NES, GFAP, and EOMES. When confluent (18-10 days after plating), the ES cells from 4 X 6cm dishes were treated with 1 mg/ml collagenase, type IV (Invitrogen/GIBCO) for 5-10 min and gently scraped off with 5 ml pipette. RNA was purified with TRIzol Reagent from Invitrogen. Protocol ref, Genome Res. 11: 153-1558 (2001). [PMID:11544199]) Double-stranded CDNAs were synthesized with an Oligo(dT) primer [Invitrogen:	5 PGACTRGATCGGGGGGGGGCGCCTTTTTTTTTTTTTTTTTT	Query Match  13.1%; Score 733.4; DB 6; Length 819;  Best Local Similarity 94.6%; Pred. No. 1.6-107;  Matches 769; Conservative 0; Mismatches 43; Indels 1; Gaps 1;  Qy 3891 AGGAGATACACAAAGAAGCTAGTCCCAATCGAATCAGATAGAAGATCTTCATTTGA 3950  Db 1 AGAGGTAATCCCAAAGAAGCTAGTCCCAATCGAATCAGAAGATTAGAAGATCTTCATTTGA 60	QY         3951 AAACCATCTACCTCAGCATTTACTGAGCATTTTAAAACTCCAGCAGAGATGTCTTT 4010           Db         61 AAACCATCTACCTCAGCATTTACTGAGCATTTTAAAACTCAGCTTCACAGAGATGTCTTT 120           QY         4011 GTGATGTGATGCTTAGCAGTTTGGCCCGAAGAAAGGAAAATATCCAGTACCATGCTTTT 4070           Db         121 GTGATGTGATGTTAGCAGTTTGGCCCGAAGAAGGAAAATATCCAGTACCATGCTTTT 4070           Db         121 GTGATGTGATGCTTAGCAGTTTGGCCCGAAGAAGGAAAATATCCAGTACCATGCTGTTTT 180
	GECTTTGTGATGTTGATGTTTGGCCCGAAGAAGAAATTTCAGTACCATGC TGTTTTGTGATGTGA	425 ATCTTTTATADADAGGCTCACTGACAGAGACGCTGTTATTTCCCACAGCAATCAT 481  424 TGCAGACTAACTTTATTAGGAGAGACGAGCGAGGAGGAGTGATTGCCACAGCAATCAT 481  482 TGCAGACTAACTTTATTAGGAGAAACCTATGCCAGCTGGGAGTGATTGCTAAGAGGCTCC 4304  482 TGCAGACTAACTTTATTAGGAGAAACCTTTTGCTAAGAGGCTCC 541  485 AGTCTTTGCATTCCAAAGCCTTTTGCTAAAGTTTTGCACTTTTTTTT		12 0 CD652380 819 bp mRNA linear EST 18-JUN-2003 ION AGENCOURT 14537640 NIA Human H1 Embryonic Stem Cell CDNA Library (Long) Homo sapiens CDNA clone IMAGE:30421320 5', mRNA sequence. ON CD652380 CD652380.1 GI:31889706 S EST.	Σ ωω

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Ilbases 1 to 826)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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                           241 GTTGAGCAGCTCTGAACTGATTTTACTTTTAAAGAATTTGCTCATGGACCTGTCATCCTT
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/ lab host="nhing (T1-phage-resistant)"
/ clone="lab."
/ lab host="nhing (T1-phage-resistant)"
/ clone="vector: pDNN=Lib; Site 1: Sfil (ggccattatggcc);
/ note="vector: pDNN=Lib; Site 1: Sfil (ggccattatggcc);
/ note="vector: pDNN=Lib; Site 1: Sfil (ggccattatggcc);
/ site 2: Sfil (ggccgcctggcc); Double-stranded CDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder-2%, blood - 33.4%, brain - 5.6%, brast - 12.5%, colon-4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3% and skin - 2.3%, prostate - 4.3%, salivary gland - 1.3% and skin - 2.3%, salivary was constructed using the Clontech cractor SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH MGC Library."
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Pred. No. 1e-106;
0; Mismatches 17; Indels
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Best Local Similarity 97.0%;
Matches 796; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 795)

1 Harrington, J.J.; Sherf, B., Rundlett, S., Jackson, P.D., Ferry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costaizo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Creation of genome-wide protein expression libraries using random
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RST13466 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ATATTICCCAGAAGGAGGATACACAAAGAAGCTAGTCCCAATCGAATCAGAGTATAGAAG 183
                                                                                                                                                                                                      244 AGAGATGTCTTTGTGATGTGATGCTTAGCAGTTTGGCCCGAAGAAGGAAAATATCCAGTA 303
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                                                                                                               184 Arctrcatrigaaaaccarctaccrcagcarctacgaggarrtraaaacrcagcricac
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3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Email: scain@athersys.com
High quality sequence stop: 441.
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/mol_type="mbkk"
/db_xref="txxon:9606"
/db_xref="txxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/note="See" (Treation of Genome-wide Protein Expression
/inbraries using Random Activation of Genome-wide Protein Expression
Libraries using Random Activation of Genome Expression
/inbraries using Random Activation of Genome a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                            662
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 773)
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RST15540 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG196325
GCCAGCAAAC-TTTCTTTGTAAAAGGCTGGTTAGTAAATTATTGCAGGCCACCTG-TGTC
                                                                                                                                                         TTTCAAACAACCCTCTAA
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3201 Carnegie Ave, Cleveland, OH 44115,
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
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                                                                        /mol_type="minsta" colored with the property of the profession of 
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                                                       'organism="Homo sapiens"
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The invention relates to a novel isolated human N-acetylglucosamine-1-phosphotransferase (GloRAc-phosphotransferase) (I) and phosphodiester alpha-GloRAcase (N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase) (II). The protein of the invention has nephrotropic activity, and may be useful in enzyme replacement therapy. A protein of the invention (I), (II) is useful for preparing a phosphorylated lysosomal hydrolase. The phosphorylated hydrolase comprising a terminal mannose-6-phosphate, is useful for treating a

Disclosure; Page 26-28; 62pp; English.

242 7 ADD26807 178 6 ABU11844 113 4 ABU11844 113 7 ADD21827 113 7 ABW01494 113 7 ABW01494 113 7 ABW01494 113 7 ABW01494 652 4 ARBS9094 652 7 ABM5193 502 7 ABW01544 67 8 ABW59064 67 8 ABW59064 67 8 ABW59064 68 4 AAW31616 68 4 AAW31616 69 4 AAW31616	Add26807 Human adi	9857 Protei	Abr61382 Partial r	Add27822 Rat alpha	Abw01494 Partial r	Abw01543 Partial r	Adg39859 Protein B		Abr61383 Partial D	Add27824 Fruit fly	Abw01495 Partial f	Abw01544 Partial f	Abo59064 Human gen	Adi21059 Novel hum	Abb38187 Peptide #	Aam31616 Peptide #	Aam71337 Human bon	Aam58821 Human bra	Abg53045 Human liv
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Novel N-acetylglucosamine-1-phosphotransferase and N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase, useful for producing phosphorylated lysosomal hydrolase for treating lysosomal storage diseases.
                                                                                                   Human; N-acetylglucosamine-1-phosphotransferase; nephrotropic; GlcNAc-phosphotranferase; phosphodiester alpha-GlcNAcase; N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase; enzyme replacement therapy; phosphorylated lysosomal hydrolase; lysosomal storage disease; enzyme; alpha-subunit.
                                                                                Human GlcNAc-phosphotransferase alpha-subunit.
                                                                                                                                                                                                                                                                                                  (GENZ-) GENZYME GLYCOBIOLOGY RES INST INC.
           ABR61376 standard; protein; 928 AA.
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The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble Glowac-phosphotransferase (UDP-N-acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease. The present sequence represents the amino acid sequence of the human Glowac-phosphotransferase alpha subunit.
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                                                                                                                                            The invention relates to a method for producing a high mannose glycoprotein. The method comprises: introducing and expressing a polynucleotide encoding a glycoprotein into a mammalian cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of decxymannojirimycin and kifurensine to inhibit glycosylation of the glycoprotein; and collecting the glycoprotein. The invention is useful igene therapy. The method is useful for producing a high mannose glycoprotein in a complex carbohydrate deficient cell for treating appropriation of the glycoprotein in a complex carbohydrate deficient cell for treating accepting its storage disease. The present sequence is human N-accepting cosamine-1 (GlcNAc)-phosphotransferase alpha subunit precursor protein
Producing a high mannose glycoprotein for treating lysosomal storage disease, comprises culturing the lectin resistant mammalian cell in the presence of deoxymannojirimycin and kifunensine.
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   AGKSFONRLCLPMPIDVVYTWVNGTDLBLLKELQQVREQMEEEQKAMREILGKNTTEPTK
                                AGKSFONRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEBQKAMREILGKNTTEPTK
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                                                      GDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQEKQVHKSILPNSLG
                                                                                                                                                                                PLESQMTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKYF
 EAEILFBDI PKEKR FPKFKRHDVNSTRRAQEEVKI PLVNI SLLPKDAQLSLNTLDLQLEH
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                                                                                             VSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQKTIGGNVTKEKPPSLIV
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N-acetylglucosamine-1-phosphotransferase; enzyme; gene therapy; human.
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Best Local Similarity 100.0%;
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Human nucleic acid-associated protein (NAAP-9). Ä. standard; protein; 1256 (first entry) 30-OCT-2002 **34444444** 

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Human, nucleic acid-associated protein, NAAP-9, neurological disorder, arteriosclerosis, cancer, cell proliferative disorder, atherosclerosis,

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lymphoma; epilepsy; Alzheimer's disease; developmental; anticonvulsant; utolimune disorder; ALDS; allergy; anaemia; stroke; malaria; leishmania; gene therapy; nootropic; neuroprotective; cerebroprotective; virucide; immunosuppressive; protozoacide; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acid-associated proteins (NAAP) and nucleic acids. The nucleic acid and anino acid sequences are useful for diagnosing, treating and preventing cell proliferative e.g. arteriosclerosis, atherosclerosis, lymphoma or cancers), neurological (e.g. epilepsy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. ALDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful gene therapy. The present sequence is human NAAP-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ramkumar J, Yao MG, Policky JL;
H, Batra S, Ding L, Lal PG;
K, Griffin JA, Xu Y, Azincai Y;
BA, Mason PM, Burford N, Hafalia AJA;
Emerling BM, Marquis JP, Lee SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGKSFONRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEEQKAMREILGKNTTEPTK
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                                                                                                                                 448. .469
/note= "Notch domain"
500. .536
/note= "Notch domain"
1018. .1030
/note= "EF-hand calcium-binding domain"
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                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      21-DEC-2000; 2000US-0257714P.
05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262802P.
23-JAN-2001; 2001US-0263823P.
02-FBB-2001; 2001US-0266088P.
29-OCT-2001; 2001US-0348442P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baughin MR, Lu Y, Arvizu C,
Walia NK, Tribouley KM, Yue
Borowsky ML, Lu DAM, Gandhi
Gietzen KJ, Tang YT, Warren
Lee EA, Yang J, Gorvad AE,
                                                                                                                                                                                                                                                                                                                        2001WO-US050256
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Swarnakar A, Reddy R;
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                                                                                    Homo sapiens
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884
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                                             635 AQKGYENLVSPITLLPEAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLP
                                                                                                         KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVA
                                                                                                                                                KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVA
                                                                                                                                                                                                                      POEKOVHKSILPNSLGVSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQK
                                                                                                                                                                                                                                                                         POEKQVHKSILPNSLGVSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQK
                                                                                                                                                                                                                                                                                                                                      TIGGNVTKEKPPSLIVPLESQMTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannose glycoprotein, gene therapy; carbohydrate deficient cell; lysosomal storage disease, N-acetyiglucosamine-1-phosphotransferase; gastrointestinal; enzyme; lectin resistant cell; deoxymannojirimycin; kifunensine; glycosylation inhibition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  925
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N-PSDB; AAD62490.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRDQYHVLFDSYRDNIAGKSFQNRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEEQ 104
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Pred. No. 0;
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99.3%;
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Glycoprotein; lectin; lysosomal storage disease; gastrointestinal; N-acetylglucosamine-1-phosphotransferase; gene therapy; enzyme.

N-acetylglucosamine-1(GlcNAc)-phosphotransferase protein.

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                            Mismatches
   Score 4630;
Pred. No. 0;
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            al Similarity 99.3
875; Conservative
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Query Match
Best Local
Matches 87
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culturing

Producing a glycoprotein with reduced complex carbohydrates by culting the lectin resistant mammalian cell expressing the glycoprotein for treating lysosomal storage disease.

21-DEC-2001; 2001US-00023890.

NOVAZYME PHARM INC

(NOVA-)

2001US-00023890

21-DEC-2001;

03-JUL-2003

US2003124653-A1.

Unidentified

8; Page 10-13; 46pp; English

Claim

treating lysosomal storage

WPI; 2003-810985/76. N-PSDB; AAD62649.

Canfield WM;

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                                                                                                                                                                                                                                                                                                                                                The present invention provides a method of producing a glycoprotein having reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is N-acetylglucosamine (GlcNAc)-
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Pred. No. 0;
2; Mismatches
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Best Local Similarity 99.3%;
Matches 875; Conservative ;
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standard; protein;

ABW01536

RESULT

ABW01536

ABW01536
ID ABW0
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DT 15-J

entry)

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15-JAN-2004

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Human; nucleic acid-associated protein, NAAP-13; neurological disorder; arteriosclerosis; cancer; cell proliferative disorder; atherosclerosis; lymphoma; epilepsy; Alzheimer's disease; developmental; anticonvulsant; autoimmune disorder; ALDS; allergy; anaemis; stroke; malaria; leishmania; gene therapy; noctropic; neuroprotective; cerebroprotective; virucide; immunosuppressive; protozoacide; antimicrobial.
                                               515 VLSCGFDAGDCGQDHFHELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNP 574
                                                                                           644
                                                                                                           I RHASIANKWKTIHLIMHSGMWATTIHFNLTFQNINDEEFKMQITVEVDTREGPKLNST 634
GGDCSGNSGGSRYIAGGGGTGSIGVGQPWQFGGGINSVSYCNQGCANSWLADKFCDQACN 514
                             VLSCGFDAGDCGQDHFHELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNP 584
                                                                                                                                                      AQKGYENLVSPITLLPEAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLP 704
                                                                                                                                                                                    694
                                                                                                                                                                                                                  KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVA 764
                                                                                                                                                                                                                                          KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVA 754
                                                                                                                                                                                                                                                                             PQEKQVHKSILPNSLGVSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQK 824
                                                                                                                                                                                                                                                                                               PQEKQVHKSILPNSLGVSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQK 814
                                                                                                                                                                                                                                                                                                                                         TIGGNVTKEKPPSLIVPLESQMTXEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHY 884
                                                                                                                                                                                                                                                                                                                                                                   TIGGNVTKEKPPSLIVPLESQMTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHY 874
                                                                                           I I RHASI ANKWKTIHLIMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNST
                                                                                                                                                                                 AQKGYENLVSPITLLPRAEILFEDIPKEKRPFKFKRHDVNSTRRAQEEVKIPLVNISLLP
                                                                                                                                                                                                                                                                                                                                                                                                                       TDSYLGFLPWEKKKYFLDLLDEEESLKTQLAYFTDSKNRAR 915
                                                                                                                                                                                                                                                                                                                                                                                                    TDSYLGFLPWEKKKYFQDLLDEEESLKTQLAYFTDSKNTGR 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human nucleic acid-associated protein (NAAP-13)
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/note= "Transmembrane domain"
1176. .1196
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/note= "Transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cytosolic domain"
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/label= Signal peptide
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21-DEC-2000; 2000US-0257714P.

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nucleic acids. The nucleic acid and amino acid sequences are useful for diagnosing, treating and preventing cell proliferative e.g. atteriosclerosis, lymphoma or cancers), neurological (e.g. epilepsy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. AIDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful in gene therapy. The present sequence is human NAAP-13
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                                                                                                                                                                                                                                                                                                                     Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS).
                                                                                                                                          Ramkumar J, Yao MG, Policky JL;
H. Batra S, Ding L, Lal PG;
AR, Griffin JA, Xu Y, Acinzai Y;
BA, Mason PM, Burford N, Hafalia AJA;
Emerling BM, Marquis JP, Lee SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AGKSFONRLCLPMPIDVVYTWVNGTDLELLKELQOVREQMEEEQKAMREILGKNTTEPTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPTFKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNKQTKKNMT1DGKELT1SPA
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                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to nucleic acid-associated proteins (NAAP) and
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                                                                                                                                                                                                                                                                                                                                                                                                Claim 68; Page 169-172; 193pp; English.
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                                                                                                                                                                           ML, Lu DAM, Gandhi
KJ, Tang YT, Warren
Yang J, Gorvad AE,
                                                                                                                                              Arvizu C,
05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262302P.
23-JAN-2001; 2001US-026823P.
02-FSB-2001; 2001US-0266882.
29-OCT-2001; 2001US-0348442P.
                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                                                                                                        Baughin MR, Lu Y, Arviz
Walia NK, Tribouley KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 867; Conservative
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              The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
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                                                                                                                           Length 846;
                                                                                                                                                   Indels
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                                                                                                                           . 9
                                                                                                                           В
                                                                                                                         Score 4468; DE
Pred. No. 0;
1; Mismatches
                                                                                                                        Query Match
Best Local Similarity 99.8%;
Matches 844; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides encoding full-length polypeptides, e.g. secretory or membrane proteins, useful for developing medicines for diseases the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otsuki T, Wakamatsu A, Sato H, Ishii S;
Hio Y, Otsuka K, Nagai K, Irie R, Tamechika
Otsuka M, Nagahari K, Masuho Y;
                 HELYKVILLPNOTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTHL
                                                                                                         IMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLP
                                                                                                                           GDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQEKQVHKSILPNSLG
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GGGTGSIGVGHPWQFGGGINSVSYCNQGCANSWLADKFCDQACNVLSCGFDAGDCGQDHF
                                                                                                                                                               EAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLPKDAQLSLNTLDLQLEH
                                                                                                                                                                              EAEILFEDI PKEKRFPKFKRHDVNSTRRAQEBVKI PLVNI SLLPKDAQLSLNTLDLQLEH
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                                                    HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL
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(REAS-) RES ASSOC BIOTECHNOLOGY
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2002US-0350435P
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N-PSDB; ADA53185.
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24-JAN-2002;
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New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new isolated polypeptide comprising an amino acid sequence selected from 17 fully defined human NOVX sequences (even SEQ ID NOS between ADG39770 and ADG39802), a mature form of the NOVX amino acid or a variant of NOVX, where one or more amino acid residue in the variant differs in no more than 15% of the amino acid residues of NOVX. Also included are an isolated nucleic acid (NA) molecule (comprising a nucleic acid sequence encoding a NOVX polypeptide above
                                                                                                                                                           congenital heart defect; pulmonary stenosis; scleroderma; obesity; congenital heart defect; pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AIDS; bronchial asthma; Crohn's disease; multiple sclerosis; inffectious disease; ancerda; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia;
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Malyankar UM, Wasserman SM, Edinger SR;
                                                                                                                                                  cardiomyopathy; atherosclerosis; hypertension;
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                               ADG39856 standard; protein; 847 AA.
                                                                                                                    Protein similar to human NOV12 #2.
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23-APR-2001; 2001US-0285748P.
24-APR-2001; 2001US-028668P.
25-APR-2001; 2001US-0286292P.
03-MAY-2001; 2001US-0288334P.
16-MAY-2001; 2001US-0291241P.
14-SEP-2001; 2001US-0322284P.
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SPYTEK K A.
MEHRABAN F.
TOPPER J N.
MALYANKAR U M.
WASSERVAN S M.
EDINGER S R.
SMITHSON G.
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Smithson G,
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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(GUNT/) C
(KOMU/) H
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(SPYT/)
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RESULT 11
ADG39856
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cc codd SEQ ID NOS between ADG39769 and ADG39801), a nucleic acid fragment cnooding at least a portion of a NOVX polypeptide and a complement of NOVX RA), a vector comprising NOVX NA, a cell comprising the vector, an antibody that immunospecifically binds to NOVX, a method for determining the presence or amount of NOVX or NOVX NA in a sample, a method for departition an agent that binds to NOVX a method for identifying an electricity of NOVX, a method for identifying an adent for second that modulates the expression or activity of NOVX, a method for a modulator of activity or of latency or predisposition to a NOVX-associated disorder, a method for screening for a modulator of activity or of latency or predisposition to a NOVX-associated disorder, a method for the presence of or predisposition to a disease consociated with altered levels of NOVX or NOVX NA in a first mammalian subject and a method of treating a pathological state in a mammalian subject and a method of treating a pathological state in a mammalian collipse, nucleic acid or antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease or a condition associated for antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease or a condition associated for antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease or a condition associated for diabetes, metabolic disorders, pulmonary scolated cancer diabetes, including cardiomypaphy. Organizal asthma, Crohn's disease, including cardiomypaphy. Organizal asthma, Crohn's disease, including disorders, adease, hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, adenocarcinoma, fertility, haemophilia, graft versus host disease, disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease, anorexia, neurodegenerative disorders, haematopolical samples (tissue typhing), and in formanic identification of a biological samples (tissue ty
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Matches 842;
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The invention relates to an isolated polypeptide comprising any one of 17 human NOVX (1-9, 10a, 10b, 11-16) appearing as ABU07369-ABU07385, a mature form of it, or a variant of them, where one or more residues of the cather sin not more than 15 % from the residues of the sequence of them and their encoding polynucleotides appearing as ABX10223 - ABX10239. Also included are NOVX expression or modulates the antibodies, identifying an agent that binds to or modulates the expression or activity of NOVX and screening for a modulates the cather or or includes, polynucleotides and antibodies are useful in manufacturing a medicament for treating or preventing a syndrome associated with NOVX. Colory polypeptides, polynucleotides and antibodies are useful in manufacturing a medicament for treating or preventing a syndrome associated with NOVX. Colory cascolated disorder, such as cardiomyopathy, atheroselerosis, cancer, hypertension, diabetes, inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, cather immunodylobulin (Lg)A mephropathy, cirrhosis, arthritis, cancer, cather associated disorders associated with hophropathy colories, concernial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. The nucleic of small molecules that modulate or inhibit e.g. neurogenesis, colories caids and polypeptides may also be used as targets for the identification of angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or colories in munospecifically to NOVX substances for use in therapeutic or mangoling, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes, in chromosome mapping, tissue typing, preventive medicine, and probes and polypeptides are also be used as hybridisation of probes, in chromosome mapping, tissue typing, preventive medicine, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NHPAQNVDSAEVEKSGIRRGKNGCRAVSLQDWPGTRGCANFTFAFCHDCKFSEVSQKRFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 NVSVVVFDSTKDGTLLTQKVTFEWKCEEGEVASNANIWGKTDLGSPRRPLPWPVALEPPR 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- EASVALLKINNPKDFQELNKQTK 285
       treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 YILQNCHWLTDWGWTWLALLHGSLILQGPASEPGCVLLKAKVVLEWSRDQYHVLFDSYRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TKKSEKQLECLLTHCIKVPMLVLDPALPANITLKDLPSLYPSFHSASDIFNVAKPKNPST
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89.5%; Score 4391; DB 6;
Best Local Similarity 73.0%; Pred. No. 0;
Matches 884; Conservative 13; Mismatches 28;
                                                                             Claim 1; Page 94-95; 301pp; English.
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                                             pharmacogenomics.
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VSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQKTIGGNVTKEKPPSLIV
                                                                                                                                                                                                                                                                                                                                                           HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL
                                                                                IMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLP
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Malyankar UM, Wasserman S; Edinger S;
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; 2001US-0286292P.
; 2001US-0288334P.
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Gunther E,
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N-PSDB; ABX10235.
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25-APR-2001;
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Smithson G,
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KNMTIDGKELTISPAYLLWDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRN
                                                                                                 NDDVMFGKDVWPDDFYSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDG
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                                                                                                                                NDDVMFGKDVWPDDFYSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDG
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                                 KNMTIDGKELTISPAYLLWDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRN
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The invention relates to a new isolated polypeptide comprising an amino acid sequence selected from 17 fully defined human NOVX sequences (even SEQ ID NOS between ADG39770 and ADG39802), a mature form of the NOVX canno acid or a variant of NOVX, where one or more amino acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue of NOVX. Also included are an isolated nucleic acid differs of comprising a nucleic acid sequence encoding at least a portion of a NOVX polypeptide acid fragment of NOVX hat immunospecifically binds to NOVX, a method for determining the presence or amount of NOVX no NOVX, a method for identifying an agent that that binds to NOVX, a method for identifying an agent that but that binds to NOVX, a method for identifying an agent that but that binds to NOVX, a method for modulating the activity of NOVX, a method for adentifying an agent that modulates the expression or activity of NOVX, a method for determining the presence of or predisposition to a disease of a conjusted with altered levels of NOVX or NOVX NA in a first mammalian cutivity or of latency or predisposition to a NOVX-associated disorder. The NOVX polypetides and nucleic acid or antibody that binds to NOVX. The NOVX or an antibody that binds to NOVX. The NOVX or an antibody that binds to NOVX. The NOVX acid acids or conditions associated with NOVX sequences, including cacids or conditions associated with NOVX sequences, including cacids or conditions associated with NOVX sequences, including caled with the method of treating or presence or an orditions associated with NOVX sequences, including caled with the NOVX attenting and part defects, pulmonary thereosciences is not or an ordition or associated with not a dispense or a not conditions associated with NOVX sequences, including caled with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spytek KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ысь кы, Padigaru M, Kekuda R, Spytek KA.
Malyankar UM, Wasserman SM, Edinger SR;
Komuves L;
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                                                                                                                                              20-APR-2001; 2001US-0285609F.
23-APR-2001; 2001US-0285748F.
24-APR-2001; 2001US-0286629F.
25-APR-2001; 2001US-0286292F.
03-MAY-2201; 2001US-0298334F.
16-MAY-2001; 2001US-029241F.
14-SEP-2001; 2001US-0322241F.
                                                                                                         11-APR-2002; 2002US-00120801
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Gunther E,
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SPYTEK K A.
MEHRABAN F.
TOPPER J N.
MALYANKAR U M
WASSERMAN S M
EDINGER S R.
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                       SHIMKETS R A.
PADIGARU M.
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Smithson G,
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                                                                                                                                                                                                     FRRHDVNSTRRAQEEVKIPLVNISLLPKDAQLSLNTLDLQLEHGDITLKGYNLSKSALLR
                                                                                                                                                                                                                                                                                                                                                                                               BNSRMBENAENHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKYFQDLLDEBESLKTQLAYF
                                                                     PKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHLIMHSGMNATTIHFNLTF
                                                                                                                                        QNTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLPEABILFEDIPKEKRFPK
          LSCGFDAGDCGQENSDSKNRKTEEKCPVKKKKIMFLFFPLDHFHELYKVILLPNQTHYII
                                           PKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHLIMHSGMNATTIHFNLTF
                                                                                                            QNTNDEBFKWQITVEVDTREGPKLNSTAQKGYENLVSPITLLPEAEILFEDIPKEKRFPK
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N-PSDB; ACC81007.
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obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS, bronchial asthma, Crohn's disease, multiple sclerosis, infectious disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), immune disorders, haematopoietic disorders, dyslipidaemias, and wasting disorders associated with chronic diseases. The polypeptides can be used as immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mapping, identifying individual from minute biological samples (tissue typing), and in forensic identification of a biological sample. The present
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alpha-GlcNAcase (N-acetylglucosamine-i-phosphodiester alpha-N-Acetylglucosaminidase) (II). The protein of the invention has protein of the invention has protein of the invention (I). (II) is useful for preparing a phosphorylated lysosomal hydrolase. The phosphorylated hydrolase comprising a terminal mannose-6-phospher, is useful for treating a patient suffering from a lysosomal storage disease. The prospection of the present sequence is used in the exemplification of the invention
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                                                                                                         Length 908;
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                                                                                                         79.4%; Score 3894; DB 4; 79.9%; Pred. No. 7.2e-305; ive 61; Mismatches 104;
                                                                                                                              Conservative
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Best Local Similarity
                                                                                         Sequence 908 AA;
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879
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lysosomal storage disease e.g. Fabry's disease by contacting the protein
with a soluble GlcNAc-phosphotransferase and producing a phosphorylated
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  ---KEEESDRAEGNA---VPVKELVPGRRLQ---QNYPGFLPWEKKKY
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                                                                                                                                                                                                                                                                                                                                                                    mouse; protein phosphorylation; soluble GlcNAc-phosphotransferase; UDP-N-acetylglucosamine; lysosomal storage disease; Fabry's disease;
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                                                                                                                                                                                                                                                                                                                               GlcNAc-phosphotransferase associated protein #1.
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                                                                         Disclosure; SEQ ID NO 9; 55pp; English
                                                  FODLLDEEESLKTOLAYFTDSKNTGROLK
                                                                                                                                                                                                    AA.
                                                                                                                                                                                                    ADD27817 standard; protein; 908
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                                                                                                                                                                                                                                                                                        (first entry)
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NQLKTKLPEN-LSSKVKLLQLYSEASVALLKLNNPKDFQELNKQTKKNMTIDGKELTISP 299

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420 FYSHSKQQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIA 479
241 SQLKTKLPRKAPPLKIKLLRLYSBASVALLKLNNPKGFQELNKQTKKNMTIDGKBLTISP 300
                                   LIMHSGMNATTIHFNLTFQNTNDEEFKWQITVEVDTREGPKLNSTAQKGYENLVSPITLL 659
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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Minimum DB Maximum DB

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Sequence 1. Application US/09635872A

Sequence 1. Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:

APPLICANT: CAMPIELD.

TILLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE.

FILE REPREMENCE: 1956313US0

CURRENT APPLICATION NUMBER: 00/09/635,872A

CURRENT PELING DATE: 2000-06-10

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 928
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Db 361 DNPRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDF 420	QY         421         YSHSKGQKYZLTWPVPNCAEGCPGSMIKDGYCDKACNNSACDWDGGDCSGNSGGSEXIAG         480           DD         421         YSHSKGQKYXLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSEXIAG         480	QY         481 GGGTGSIGVGHPWQFGGGINSVSYCNQGCANSMLADKFCDQACNVLSCGFDAGDCGQDHF 540           Db         481 GGGTGSIGVGHPWQFGGGINSVSYCNQGCANSMLADKFCDQACNVLSCGFDAGDCGQDHF 540	Qy 541 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL 600  541 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL 600	Qy 601 IMHSGMNATTIHFNLTPQNTNDBEFRMQITVEVDTREGPKLNSTAQKGYENLVSPITLLP 660	Qy 661 EAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLPKDAQLSLNTLDLQLEH 720	Qy 721 GDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQEKQVHKSILPNSLG 780	Qy         781 VSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQKTIGGNVTKEKPPSLIV 840           Db         781 VSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQKTIGGNVTKEKPPSLIV 840	Qy 841 PLESQWTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKYF 900  B41 PLESQWTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKYF 900	Qy 901 QDLLDEESLKTQLAYFTDSKATGRQLK 928	S S S S S S S S S S S S S S S S S S S	) R Z Z	PRIOR FILING DATE: 1999-09-14 NUMBER OF SEQ ID NOS: 52 SOFTWARE: PatentIn version 3.0 SEQ ID NO 1 LENGTH: 928	; TYPE: PRT ; ORGANISM: Homo sapiens US-09-636-077A-1	Query Match 100.0%; Score 4907; DB 4; Length 928; Best Local Similarity 100.0%; Pred. No. 0; Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 MLFKLLORQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI 60	QY 61 AGKSFQNRLCLPMPIDVVYÝWVNGTDLELLKELQQVREQMBEBQKAMREILGKNTTEPTK 120	QY 121 KSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNV 180

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                                                    1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI
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100.0%; Pred. No. 0;
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               Query Match 100.
Best Local Similarity 100.
Matches 928; Conservative
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Sequence 1, Application US/09986552

Patent No. 6670165

GENERAL INFORMATION:

APPLICANT: CANFIELD, William

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASE:

FILE REFERENCE: 215089US77DIV

CURRENT APPLICATION NUMBER: 09/635,872

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 1099-09-14

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.1

LENGTH: 228 120 120 240 240 360 480 720 NOLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNKQTKKNMTIDGKELTISPA 300 300 420 420 480 540 540 600 600 660 999 GDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQEKQVHKSILPNSLG 780 9 AGKSFQNRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEEQKAMREILGKNTTEPTK SVVVPDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPTFKET 1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPTFKET 241 NQLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNKQTKKNMT1DGKELT1SPA DNPRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDF 421 YSHSKGQKVYLIWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG 601 IMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLP DNPRVTIVTHQDVPRNLSHLPTFSSPALESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDF YSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG HELYKVILLPNOTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL 541 HELYKVILLPNOTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL IMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLP EAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLPKDAQLSLNTLDLQLEH EAEILFEDIPKEKRPPKFKRHDVNSTRRAQEEVKIPLVNISLLPKDAQLSLNTLDLOLEH Gaps .; 0 Indels DB 4; ; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 928; Conservative 0; Mismatches ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-986-552-1 721 g ò

Db 481 GGCTGSIGVGHPWQFGGCINSVSYCNQCCANSWLADKFCDQACNVLSGGFDAGDCGQDHF 540  Qy 541 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL 600  S41 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASIANKWKTIHL 600  Qy 601 INHSGMAATTHFINLFGNTNDEEFKWQITVEVDTREGPKLNSTAQKGYENLVSPITLLP 660  L	THE OF THE SELECTION WAS STATED BY THE STATE OF THE STATE
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Batent No. 6642038
BATENT INFORMATION:
APPLICANT: CANFIELD, WILLIAM M
FITLE OF INVENTION GLORAC PHOSPHOTRANSFERASE OF
FILE REFERENCE: 2101190080CONT
CURRENT APPLICATION NUMBER: US/09/636,060C
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                                        AYLLWDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLN
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TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
FILE REFERENCE: 1950-1050
CURRENT APPLICATION NUMBER: US/09/636,077A
CURRENT APPLICATION DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
SCOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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12; Conservative
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US-09-986-552-15
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CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION WUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 908
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                                                                                    TYPE: PRT
CORGANISM: Mus musculus
US-09-636-060C-15
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US-09-986-552-15

Satent No. 6670165

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 215089US77DIV

CURRENT FILING DATE: 2001-11-09

PRIOR APPLICATION NUMBER: 09/635,872

PRIOR PAPLICATION NUMBER: 09/635,872

PRIOR APPLICATION NUMBER: 09/635,872

PRIOR APPLICATION NUMBER: 09/635,831

PRIOR PILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 15

LENGTH: 908
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719	QY         600 LIMESGMARTTHHPULTEQNTNDEBFXQUITVEVDTREGPKLNSTAQKGYENLVSPITLL 659           DD         601 LIMPGGMNATTIYFNLTLQNANDEBFXLQIAVEVDTREAPKLNSTTQKAYESLVSPYTPL 660	OY 360 LDNPRVIIVTHODVFRNLSHLPTFSSPAIESHIRRIEGLSOKFIYLNDDVMFGKDVWPDD Db 361 LDNPRVIIVTHODIFSALSHLPTFSSPAIESHIRRIEGLSOKFIYLNDDVMFGKDVWPDD 361 LDNPRVIIVTHODIFQALSHLPTFSSPAIESHIRRIEGLSOKFIYLNDDVMFGKDVWPDD	SPAIESHIHRIEGLSQKFIYLNDDVWFGKDVWPDD 419 
13.10	660 PEAEILPEDIPKEKRFPKFKRHDVNSTRRAQESUKIPLVNISLLPKDAQLSLNTLDLQLE  : :-	420	
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13   Principal Continues   12   Principal Continues   13   Principal Cont	780 GVSERLQRLIFPANSVKVNGHDQGQNPPLDLETTARFRVETHTQKTIGGNVTKEKPPSLI 83  778 AGEHRSERWTAPAETVTVKGRDHALNPPPVLETNARLAQPTLGVTVSKENLSPLI 83	540	
SOURCE   CONTINUES   CONTINU	840 VPLESQMTKEKKITGKEKNSRMEENABNHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKY 89	600	
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144	SEQUENCE 15. APPLICATION US/09636596C Sequence 15. APPLICATION WILLIAM APPLICANT: CANTELD, WILLIAM TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNACase OF THE LYSOSOWAL TARGETING TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNACase OF THE LYSOSOWAL TARGETING TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNACase OF THE LYSOSOWAL TARGETING TOWNERS PEPLICATION NUMBER: 109:00-101-77 PRICE EXPERIENCE: 109:00-101-70 PRICE APPLICATION NUMBER: 06/13,831 NUMBER OF SEC DINOS: 25 SOFTWARE: PAT GOGGALIST: 090 TITLE OF NOS: 25 SOFTWARE: PAT GOGGALIST: 090 TITLE OF NOS: 25 TO 10 NO 15 TARGETING DATE: 109:00-101-101 THEATLORD TO 101-101 THEATLORD TO 101 THEATLORD TO 101-101 THEATLORD TO 101-101 THEATLORD TO 101-101	HITDE 	779 839 832 899 879 879 60

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US-09-636-060C-11
Squence 11, Application US/09636060C
Fequence 11, Application US/09636060C
Fequence 11, Application US/09636060C
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/636,060C
CURRENT PELING DATE: 1099-09-14
FRIOR APPLICATION NUMBER: 60/153,831
FRIOR APPLICATION NUMBER: 60/153,831
FRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.3
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                             Sequence 11, Application US/09636077A

Sequence 11, Application US/09636077A

Palent No. 6537785

GENERAL INFORMATION:
APPLICANT: CANFIELD, WILLIAM

TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
FILE REFERENCE: 195612USO

CURRENT APPLICATION NUMBER: US/09/636,077A

CURRENT FILING DATE: 1999-09-14

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO: 11.
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Pred. No. 1.2e-36;
4; Mismatches 4; Indels
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99; Conservative
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ORGANISM: Rattus rattus
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RESULT 12
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Sequence 11, Application US/09986552 Patent No. 6670165 GENERAL INFORMATION:

RESULT 14 US-09-986-552-11 APPLICANT: CANFIELD, William

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Sequence 11, Application US/09636596C
Patent No. 6770468
GENERAL INFORMATION:
APPLICANT: CHRIELD.
ITILE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNAcase OF THE LYSOSOWAL TARGETING PATHWAY:
FILE REFERENCE: 10929-0001-77
CURRENT APPLICATION NUMBER: 06/153,831
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: PATENTIN VETSION 3.0
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES FILE REFERENCE: 215089US77DIV CURRENT APPLICATION NUMBER: US/09/986,552 CURRENT FILING DATE: 2001-11-09 PRIOR APPLICATION NUMBER: 09/635,872 PRIOR APPLICATION NUMBER: 09/635,872 PRIOR PLING DATE: 1999-09-14 NUMBER: 60/153,831 PRIOR FILING DATE: 1999-09-14 SEQ ID NOS: 52 SOFTWARE: Patentin version 3.1 SEQ ID NO 11.
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Pred. No. 1.2e-36;
4; Mismatches 4; Indels
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Best Local Similarity 92.5%; Pred. No. 1.2e-36;
Matches 99; Conservative 4; Mismatches 4;
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l Similarity 92.5%;
99; Conservative '
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; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-636-596C-11
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; ORGANISM: Rattus rattus
US-09-986-552-11
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US-09-636-596C-11
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November 21, 2004, 12:56:09; Search time 100.171 Seconds (without alignments) 3280.691 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
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SUMMARIES		ID	US-09-895-072-1	US-09-986-552-1	US-10-023-888-4	US-10-023-889-4	US-10-023-890-4	US-10-024-197-4	US-10-023-894-4	US-10-306-686-1	US-10-023-888	US-10-023-889	US-10-023-890	US-10-024-197-2	C 400 CCC OF ULL
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Sequence 1, Application US/09895072

Sequence 1, Application US/09895072

Patent No. US20020025550A1

GENERAL INFORMATION:

ACTIVE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

FILE REPERBENCE: 210119USCONT

CURRENT PELLING DATE: 2001-07-02

PRIOR PELLING DATE: 1999-09-14

PRIOR APPLICATION NUMBER: US 09/635,872

PRIOR APPLICATION NUMBER: US 09/635,872

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 52

SOSUMARE: PATENTING PATE: 2000-08-10

SEQ ID NO. 15

SED I ô 61 AGKSFONRLCLPMPIDVVYTWVNCTDLELLKELQQVREQMEEEQKAMREILGKNTTEPTK 120 61 AGKSFQNRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEEGKAMREILGKNTTEPTK 120 KSEKQLECLITHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNV 180 09 9 1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI 1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI Gaps .; 0 DB 9; Length 928; Indels .; 0 100.0%; Score 4907; 100.0%; Pred. No. 0; ative 0; Mismatches Query Match Best Local Similarity 100. Matches 928; Conservative , ORGANISM: Homo sapiens US-09-895-072-1 TYPE: PRT 121 g ò 셤 ò

us-10-023-888-4.rapb

) TYPE: PRT ) ORGANISM: Homo sapiens US-09-986-552-1  Query Match Best Local Similarity 100.0%; Score 4907; DB 9; Length 928; Best Local Similarity 100.0%; Pred. No. 0; Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY	NRICCE-PMPIDVVYTWYNGTDLELLKELQQVREQMESEQKAMRSILGKOYTTSFTK 12 LECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNV 18 LECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNV 18 LECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNV 18 SSTKOVPBAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPIFKET 24	181 ŚVÝVFBŚTŔDVEDÁHŚGLÍKĠNSRQTVWRGYLTTDKEVPGLV 241 NQLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNK 241 NQLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNK 301 YLLWDLSAISQSKQDEDISASREDNELKYSLRSIERHAPW 301 YLLWDLSAISQSKQDEDISASRFEDNELKYSLRSIERHAPW 301 YLLWDLSAISQSKQDEDISASRFEDNEELKYSLRSIERHAPW 301 YLLWDLSAISQSKQDEDISASRFEDNEELKYSLRSIERHAPW	361 DNPRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDF 42 421 YSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG 48 421 YSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG 48 421 YSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG 48 481 GGGTGSIGVGHPWQFGGGINSVSYCNQGCANSWLADKFCDQACNVLSCGFDAGDCGQDHF 54	481 GGGTGSIGVGHPWQFCGGINSVSYCNQGCANSWLADKFCDQACNVLSCGFPAGDCGUDHF 34 541 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASTANKWKTHL 60 541 HELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRHASTANKWKTHL 60 601 IMHSGKNATTHFNLTFQNTNDEEFKAQITVEVDTREGPKLNSTAQKGYENLVSPITLLP 66 601 IMHSGKNATTHFNLTFQNTNDEEFKAQITVEVDTREGPKLNSTAQKGYENLVSPITLLP 66 601 IMHSGRNATTHFNLTFQNTNDEEFKAQITVEVDTREGPKLNSTAQKGYENLVSPITLLP 66 601 IMHSGRNATTHFNLTFQNTNDEEFKAGNTRAQUSTAGNTRAGNTAGNTAGNTAGNTAGNTAGNTAGNTAGNTAGNTAGNT	ILKGYNLSKSALLRSFLANSOHAKIKNOAIITDETNDSLYAPOENOYHKSILDNSG 78  ILKGYNLSKSALLRSFLANSOHAKIKNOAIITDETNDSLYAPOEKOYHKSILDNSG 78  ILKGYNLSKSALLRSFLANSOHAKIKNOAIITDETNDSLYAPOEKOYHKSILDNSG 78  ILKGYNLSKSALLRSFLANSOHAKIKNOAIITDETNDSLYAPOEKOYHKSILDNSG 78  ILKGRIFPPAVSYKYNGHDOGONPPLDLETTARFRYETHTOKTIGGNYTKEKPPSLIV 84  ILLI
Db   121 KSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYFSFHSASDIFNVAKPKNPSTNV 180   181 SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPFTFKET 240   181 SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPFTFKET 240   181 SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPFTFKET 240   241 NQLKTKLPENLSSKVKLLQLYSEASVALLKLNNFKDFQELNKQTKKNNMTIDGKELTISPA 300   1	361 361 421 421	4 4 0 0 0		OY 781 VSERLORLTFPAVSVKVNGHDOGONPPLDLETTARFRVETHTOKTIGGNVTKEKPPSLIV 840	RESULT 2 US-09-986-552-1 Sequence 1, Application US/09986552 Patent No. US20020150981A1 GENERAL INFORMATION: TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES TITLE OF INVENTION NUMBER: US/09/986,552 CURRENT APPLICATION NUMBER: 09/985,872 PRIOR APPLICATION NUMBER: 09/985,872 PRIOR FILING DATE: 2000-08-10 PRIOR FILING DATE: 2000-08-10 PRIOR FILING DATE: 199-09-14 NUMBER OF SEQ ID NOS: 52 SOFTWARE: Patentin version 3.1 SEQ ID NO 1 LENGTH: 928

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Sequence 4, Application US/10023889
Publication No. US20030124652A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARBO TITLE OF INVENTION: DEFICIENT CELLS
FILE REPERENCE: 2035120877
CURRENT APPLICATION NUMBER: US/10/023,889
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 21
SEQ ID NO 4
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Matches 928; Conservative 0; Mismatches
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ORGANISM: Homo sapiens
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US-10-023-889-4
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       Sequence 4, Application US/10023888
| Publication No. US2030119088A1
| GENERAL INFORMATION:
| APPLICANT: CANFIELD, William
| TITLE OF INVENTION: SOLUBLE GLCNAC PHOSPHOTRANSFERASE
| FILE REFERENCE: 203515UST US/10/023,888
| CURRENT APPLICATION NUMBER: US/10/023,888
| UNDER OF SEQ ID NOS: 38
| SOFTWARE: Patentin version 3:1
| SEQ ID NO 4
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100.0%; Score 4907;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 928; Conservative 0; Mismatches
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Publication No. US20030143669A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, Stuart
TITLE OF INVENTION: EXPRESSION OF LYSOSOWAL HYDROLASE IN CELLS EXPRESSING PRO-N-
TITLE OF INVENTION: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCCSIMANIDAS
FILE REPERBNCE: 217139US77
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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 AGKS FONRLCLPMP1DVVYTWVNGTDLELLKELQQVREQMEEEQKAMRE1LGKNTTEPTK
                                         KSEKQLECLLITHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDIFNVAKFKNPSTNV
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US-10-023-894-4
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US-10-023-888-2
| US-10-023-888-2
| Sequence 2, Application US/10023888
| Publication No. US20030119088A1
| GENERAL INFORMATION:
| APPLICANT: CANFIELD William
| TITLE OF INVENTION: SOLUBLE GLONG PHOSPHOTRANSFERASE
| FILE REFERENCE: 203515US77
| CURRENT FILING DAIE: 2001-12-21
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 2
| LENGTH: 1199
| TYPE: PRT
| ORGANISM: Pybrid
| US-10-023-888-2
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Pred. No. 0;
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                                                                                                             APPLICANT: CANFIELD, WILLIAM
TITLE OF INVENTION: PHOSHODIESTER ALPHA-GLCNAcase OF THE LYSOSOWAL TARGETING PATHWAY
FILE REPERENCE: 230397US77D10
CURRENT APPLICATION NUMBER: US/10/306,686
CURRENT FILING DATE: 2002-11-29
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Pred. No. 0;
                                                                  ; Sequence 1, Application US/10306686; Publication No. US20030148460A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 928; Conservative
                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-306-686-1
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585 IIRHASIANKWKTIHLIMHSGMNATTIHFNLTFQNTNDEBFKMQITVEVDTREGPKLNST 644	QY 405 INDDVMFGKDVWPDDFYSHSKGQKYYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWD 464
AQKGYENLVSPITLLPEAEILFEDIPKEKRPPKKRHDVNSTRRAQEEVKIPLVISLLP 7	OY 465 GGDCSGNSGGSRYIAGGGGTGSIGVGHPWQFGGGINSVSYCNQGCANSWLADKFCDQACN 524
635 ACRGIRALVSSTILLEBAREILFEBIFKERKRÄHDUNSIKKAQEEVKIPLVNISLLE 694 705 KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLANSQHAKIKNQAIITDETNDSLVA 764 605 KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLANSQHAKIKNQAIITDETNDSLVA 764 605 KDAQLSLNTLDLQLEHGDITLKGYNLSKSAIISPEDANSGHAKIKNQAIITDETNDSLVA 764	QY 525 VLSCGFDAGDCGQDHFHELYKVIILPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNP 584
POEKQUHKSILDENSELSOIIENNINEENNYHTEENNYHTIITEETINDENNY POEKQUHKSILDENSERLORITEPANSYKVNGHDOGONPPLDLETTARFRYETHTOK 8	QY 585 IIRHASIANKWKTIHLIMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNST 644
TIGGNVTKEKPPSLIVPESOMTKEKKITGKEKSNOVGEDGGGNPPLLLEITARFKVRIFIUGK TIGGNVTKEKPPSLIVPLESOMTKEKKITGKEKBNSRMEBNABNHIGVTEVLLGRKLOHY	QY 645 AQKGYENLVSPITLLPBAEILFEDIPKEKRPPKFKRHDVNSTRRAQEBVKIPLVNISLLP 704 
O IEATHGERT O	QY 705 KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLANSQHAKIKNQAIITDETNDSLVA 764
UD 8/5 IDSILGFLFWERKKIFLULLDEEESLKIQLAIFIDSKRAAK 915 RESULT 10	QY 765 PQEKQVHKSILPNSLGVSERLORLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQK 824
10-023-889-2 Sequence 2, Application US/10023889 Publication No. US20030124652A1 GENERAL INFORMATION:	QY 825 TIGGNUTKEKPPSLIVPLESQWTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHY 864 Db 815 TIGGNUTKEKPPSLIVPLESQWTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHY 874
PEPLICANT: CANFIELD, WILLIAM TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARBOH TITLE OF INVENTION: DEFICIENT CELLS TITLE OF INVENTION: DEFICIENT CELLS THE REPERBENCE: 2035120477 CURRENT APPLICATION NUMBER: US/10/023.889	OY 885 TDSYLGFLEPWEKKKYFQDLLDEBESELKTQLAYFTDSKUTGR 925
CURRENT FILING DATE: 2001-12-21  NUMBER OF SEQ ID NOS: 21  SOFTWARE: Patentin version 3.1  SEQ ID NO 2  LENGTH: 1199	
TYPE: PRT ORGANISM: hybrid S-10-023-889-2	
Query Match  94.4%; Score 4630; DB 14; Length 1199;  Best Local Similarity 99.3%; Pred. No. 0;  Matches 875; Conservative 2; Mismatches 4; Indels 0; Gaps 0;	; FILE REFERENCE: 203510US77; CURRENT FILIN DATE: 203510US77; CURRENT PAPLICATION NUMBER: US/10/023,890 ; CURRENT FILING DATE: 2001-12-21
QY 45 SRDQYHVLFDSYRDNIAGKSFQNRLCLPMPIDVVYTWVNGTDLELLKELQQVREQMEEDQ 104	
Qy 105 KAMREILGKWTTEPTKKSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSA 164	TYPE: PRT ORGANISM: hybrid S-10-023-890-2
165 SDIFNVAKPKNPSTNVSVVVFDSTKDVEDAHSGLLKGNSRQTVRRGYLTTDKEVPGLVLM 2	Query Match Best Local Similarity 99.3%; Pred. No. 0; Matches 875; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
ODLAFLSGFPPTFKETNOLKTKLPBNLSSKVKLLOLYSEASVALLKLNNPKDFQELNKQT 	
KKANMTIDGKELTISPAYLLWDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWYR 3	QY 105 KAMREILGKUTTEPTKKSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSA 164

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                                                              QDLAFLSGFPPTFKETNQLKTKLPENLSSKVKLLQLYSEASVALLKLNNPKDFQELNKQT
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Publication No. US20030133924A1

GENERAL INFORMATION

APPLICANT: CANFIELD, William

TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND NOT TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND NOT TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND NOT TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND NOT TITLE OF INVENTION: HIGHLY PHOSPHORYLATION NUMBER: US/10/024,197

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 27

SEQ ID NO S. 27
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CURRENT APPLICATION NUMBER: US/10/023,894
CURRENT FILING DATE: 2011-12-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1199
TYPE: PT
TYPE: PT
ORGANISM: hybrid
US-10-023-894-2
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FILE REFERENCE: 21402-340

CURRENT FILING DATE: 2001-04-23

FRIOR APPLICATION NUMBER: 60/28608

FRIOR APPLICATION NUMBER: 60/28608

FRIOR PILING DATE: 2001-04-24

FRIOR PILING DATE: 2001-04-25

FRIOR PILING DATE: 2001-04-25

FRIOR PILING DATE: 2001-04-25

FRIOR PILING DATE: 2001-05-03

FRIOR PILING DATE: 2001-05-04

FRIOR DATE: 2
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Pred. No. 0;
1; Mismatches 1; Indels
; Sequence 88, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
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Best Local Similarity 99.89
Matches 845; Conservative
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; ORGANISM: human
US-10-120-801-88
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Search completed: November 21, 2004, 13:22:34 Job time : 104.171 secs
LENGTH: 846
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                                    GGGTGSIGVGHPWQFGGGINSVSYCNQGCANSWLADKFCDQACNVLSCGFDAGDCGQDHF
                                                                                                                                  GGGTGSIGVGQPWQFGGGINSVSYCNQGCANSWLADKFCDQACNVLSCGFDAGDCGQDHF
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                                                                                                                                                                                                                IMHSGMNATTIHFNLTFQNTNDEEFKWQITVEVDTREGPKLNSTAQKGYENLVSPITLLP
                       DNPRVIIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGESQKFIYLNDDVMFGKDVWPDDF
                                                                      YSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAG
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APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SANO, YUNKO
APPLICANT: SONO, YUNKO
APPLICANT: HO, YUNK
APPLICANT: HO, YUNK
APPLICANT: HO, YUNK
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: REE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: YOSHKANA, TSUTOMU
APPLICANT: YOSHKANA, TSUTOMU
APPLICANT: YOSHKANA, TSUTOMU
APPLICANT: MAGCHAN, MOTOVUKI
APPLICANT: MAGCHAN, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REPERENCE: 044335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PALECTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2392, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ISCGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
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                                                                                                                                      1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLEWSRDQYHVLFDSYRDNI
                                                                   Length 846;
                                                                                                     Indels
                                                                 Score 4468; DB 14;
Pred. No. 0;
                                                                                                     ä
                                                                                                     1; Mismatches
                                                                   Query Match
Best Local Similarity 99.8%;
Matches 844; Conservative
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2392
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November 21, 2004, 12:39:03 ; Search time 28.3503 Seconds (without alignments) 3149.495 Million cell updates/sec
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4907 -
1 MLFKILQRQTYTCLSHRYGL.....SLKTQLAYFTDSKNTGRQLK 928
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hypothetical prote	cal prot	cal prot	capsule	cpsY	probable UDP-qluco	calr	ဂ	cell-fate determin	homeotic protein 1	protein	-1 protei	뚪		notch4 - mouse	ğ	B protein		-	notch homolog - se		1	protein - yea	zh protein		merozoit	merozoi	rotein pre	sal pro
DB ID	. H	T347	T3470	æ	G7053		S4	T3020	A491	S064	S181	A46	8426	S785	T090	A488	A491	8453	B491	T310	A4004	S70	S5066	A3584	8698	A2686	A5449	Ø	T3470
Length D	1	w	_	545	~	~	m	352	_	429	531	_	437	321	964	861	~	318	7	531	555	ın	755	524	755	701	701	295	0
% Query Match	٠.		٠	5.4	•	•	٠	•	•	•		3.3									٠							٠.	
Score	٠.	22.	$\neg$	266	25	55.	•	75.	68.		165	ø	62.	4.	Ŋ	4	4	4	•	4	'n	144.5	0	133	7	136.5	'n	133	133.5
Result No.	п	(1)	m	4	ហ	φ	7	00	σı	10	. 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

histidine kinase h phage-related prot type I restriction chromatin remodell probable major sur hypothetical prote major merozoite su probable tail-host notch protein - fr protein V (forv) h hypothetical prote DNA mismatch repai TyB protein - yeas hypothetical prote TyB protein - yeas protein kinesin F2	996 #text_change 09-Jul-2004	a novel basic domain-leucine zipper tr :8001130 NID:g625041; PIDN:AAA65688.1; PID:g6250	DB 2; Length 384; e-38; 71; Indels 21; Gaps 6;	PBABILFEDIPKEKRFPKFKRHDVNSTRRAQEBVKIPLVNISLL 703  : ::   :        :     :	KDAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLV 763  :  :  :	PQEKQVHKSILPNSLGVSERLQRLTFPAVSVKYNGHDQGQNPPLDLETTARFRVETHTQ 823 	KTIGGNVTKEKPPSLIVPLESOMTKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLOH 883  -   -   -   -   -   -   -   -   -   -
T08875 C097038 T069463 T069463 A24594 A24504 T16695 T06695 T06695 T07206 T47335 T09204 T0112 S50433 S5083 S52894	ALIGNMENTS ment) se) sion 09-Mar-1	ene kr encodes 95094266; PMID 0; GB:L36434;	Score 734.5; Pred. No. 2.1e 28; Mismatches	NLVSPITLLPEAEILFEDIPKEKRFPK :	DITLKGYNLSKSALLR 	SERLQRLTFPAVSVKV   :      :     EHRSERWTAPAETVTV	KTIGGNVTKEKPPSLIVPLESQMTKEKKITGKEK  :     :
00000000000000000		ion g MUID: Q6134	% % 	LPEA 	EHG ERG	LGV.	IVP.
1969 2052 2052 1642 1642 1639 1639 1756 756 756 756 1755 1755 1755	- mouse NA1 us (hous sequence,	ia.	15.0% / 57.9% rvative	CVSPITL	NTLDLOLI :       SNLDLOLI	KSILPNS:	CEKPPSL.
	protein - m names: cDNA1 Nus musculus (ar-196 #seq 1.19528	1034, 19 buse segnaber: A5 19528 lminary b: mRNA 184 <res< td=""><td>similarity 55; Conserv</td><td>TAQKGYENLVSPITLL           :        TQKAYESLVSPVTPL</td><td>PKDAQLSLI   :  :  PKEAQVRLA</td><td>APQEKQVHKS      VPQENPSHRR</td><td>TIGGNVT)</td></res<>	similarity 55; Conserv	TAQKGYENLVSPITLL           :        TQKAYESLVSPVTPL	PKDAQLSLI   :  :  PKEAQVRLA	APQEKQVHKS      VPQENPSHRR	TIGGNVT)
1333.5 1333.5 1331.5 1311.5 1233.1 1235.1 1237.5 1237.5 1237.5 1237.5 126.5	1 tical pr nate name es: Mus es: Mus sion: Mar	1025-1 The mc ence num sion: I4 s: preli ule type ues: 1-3	atch cal	644 T 3 T	704 F     63 F	764 A	824 K
	RESULT 1 149528 Nypothetical Nypothetical Nypothetical C;Species: Wu C;Date: 09-Ma C;Cotdes: No	Cell 79, 1025-1014, 1994 A/Title: The mouse segment A/Reference number: A5520f A/Accession: I49528 A/Status: preliminary A/Molecule type: mRNA A/Residues: 1-384 <res> A/Cross-references: UNIPRC</res>	Query M Best Lo Matches	දුරු	કુ	상 임	oy da

hypothetical protein SCIC3.11 SCIC3.11 - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: O5-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004 C; Accession: T34703 R; Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, May 1998 A; Reference number: Z21554 A; Reference number: Z21554

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325 MFFGRPLKASMFFS 338
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                                                                                                                                                                                    90; Conservative
                                                                                                                                                                Similarity
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                                                                                                                                           Query Match
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Matches 9
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hypothetical protein SCIC3.09 SCIC3.09 - Streptomyces coelicolor

C)Species Streptomyces coelicolor

C)Species Streptomyces coelicolor

C)Species Streptomyces coelicolor

C)Species Streptomyces coelicolor

C)Bate: 05-NOv-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C)Accession: T34701

R)Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

R)Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

R)A; Reference number: 221554

A; Reference number: 221554

A; Rocession: T34701

A; Residues: DAA

A; Residues: 1-541 < OLL>
A; Residues: L-541 < OLL>
A; Residues: UNIPROT: 069851; EMBL: ALO23702; PIDN: CAA19233.1; GSPDB: GN00070; SCOED

C; Genetics:

A; Gene: SCOEDB: SCIC3.09
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                                                           EMBL:AL023702; PIDN:CAA19235.1; GSPDB:GN00070; SCOED
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                                                                                                                                                                                                                                                      290 IDGKELTISPAYLIW--DLSAISQSKQDEDISASRFEDNEELRYSIRSIERHAPWVRNIF 347
                                                                                                                                                                                                                                                                             350 INGQIPSWLNLDNPRVTIVTHODVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDV
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                                                                                                                                                                                                             6
                                                                                                                                                                Length 586;
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Best Local Similarity 39.2%; Pred. No. 7.5e-12;
Matches 67; Conservative 31; Mismatches 63; Indels
                                                                                                                                                                                                             33; Indels
                                                                                                                                                                  Query Match
6.6%; Score 322.5; DB 2;
Best Local Similarity 46.3%; Pred. No. 2.5e-12;
Matches 62; Conservative 30; Mismatches 33;
preliminary; translated from GB/EMBL/DDBJ
                  A,Molecule type: DNA
A,Residues: 1-586 <OLL>
A,Cross-references: UNIPROT:069853;
A,Experimental source: strain A3(2)
C,Genetics:
A,Gene: SCOEDB:SCIC3.11
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Chaccession: 47-041-1250 #sequence_revision 1/-041-1258 #sext_Change 03-041-2004

R. Chaccession: 470536

R. Davies, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Natures 393, 537-544, 1998

A. Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A. Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987; PMID: 9634230

A. A. Caccession: G70536

A. Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA

A; Residues: 1-532 <COL>
A; Resid
A,Wolecule type: DNA
A,Residuces: 1-545 cPAR-
A,Gross-references: UNIPROT:Q9UWW8; GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB8351
A,Experimental source: serogroup A, strain Z2491
A,Gene: sacB; NWA0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 PRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G70536
probable cpsY protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 VNEIWTDLFSIAHVDMKLSTDRTLSSSISQFWFRLEFCKEDKDFI-----LFPTANRYSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201 KLWKH---SIKNNQLFKEG-----IRNYSEISSLPYEEDHNFDIDLVFTWVNSEDKNWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 LSAISQSKQD---EDIŞAŞRFEDNEELRYSLRŞIERHAPWVRNIFIVTNGQIPSWLNLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 LPANITLKDVPSLYPSFHSASDIFNVAKPKNPSTNVSVVVFDSTKDVEDAHSGLLKG-NS
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                                                                                                                                                                                                                                                                                                                                5.4%; Score 266; DB 2; Length 545; 27.8%; Pred. No. 7.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     370 SNGIAKLRIEAWGNVNGECTEGEP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 HSKGOKVYL-TWPVPN--CAEGCP 443
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Notch homolog protein - sea squirt (Halocynthia roretzi)
C;Species: Halocynthia roretzi
C;Species: Halocynthia roretzi
C;Species: Halocynthia roretzi
C;Date: 02-8ep-2000 #sequence_revision 02-8ep-2000 #text_change 08-Sep-2002
C;Accession: T30201
R;Hori, S.; Saitoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A;Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the A;Reference number: Z20775
A;Accession: T30201
A;Accession: T30201
A;Molecule type: mRNA
A;Residues: 1-2352 <HOR>
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A;Genetics:
G;Superfamily. .....
                                                                                             ASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLNLD-NPRVTIVTHQDVFRNLS 378
                                                                                                                              706 DAQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAP 765
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                                              43 INADANLASLTENVLPNFPIDVVFTWVDNTDKAWQEQYYRTLQPIDQ----EDIGLYATD 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 CAEGCPGSWIK-DGYCDK--ACNNSACDWDGGDCS-GNSGGSRYIAGGGGTGSIGVGHPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KFKRHDVNSTRRAQEEVKIPL------VNISLLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494 QFGGGINSVSYCNQGC-----ANSWLADKFCDQACNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1361 QDG-----HCDEHCNNEDCLHDGMDCATPVGBCNPKYEKYCNEYYNNDYCDQGCNNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 GGFDAGDCGQDH---FHELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNP
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20.3%; Pred. No. 0.034;
tive 70; Mismatches 190; Indels 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                        HLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYSHS
                                                                                                                                                                                                                                      LNNPKDFQELNKQTKKNMTIDGKELTISPAYLLWD---
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Best Local Similarity 20.3$
Matches 112; Conservative
                                                                                                  320
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                                                         probable UDP-glucose-4-epimerase [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Accession: D87185
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Ritle: Massive gene decay in the leprosy bacillus.
A;Ritle: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <STO>
A;Cross-references: UNIPROT:Q50025; GB:AL450380; NID:g13093740; PIDN:CAC31164.1; GSPDB:G
C;Genetics:
A;Gene: cpsY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appothetical protein - Neisseria meningitidis
hypothetical protein - Neisseria meningitidis
C;Species Neisseria maningitidis
C;Species Neisseria maningitidis
C;Species Neisseria maningitidis
C;Species Neisseria meningitidis
C;Accession: $42434
K;Hammerschindt, s.; Birkholz, C; Zaehringer, U.; Robertson, B.D.; van Putten, J.; Ebell Mol. Microbiol. 11, 885-896, 1994
A;Title: Contribution of genes from the capsule gene complex (cps) to lipooligosaccharid A;Reference number: $42430; MUID:94293762; PMID:8022265
A;Accession: $4344
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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A;Residues: 1-373 <HAM>
A;Cross-references: UNIPROT:Q51151; EMBL:L09188; NID:g388931; PIDN:AAA63160.1; PID:g3885
A;Experimental source: strain B1940
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALLKLNNPK--DFQELNKQTKKNMT-----IDGKELTISPAYLLWDLSAISQSKQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRILEPIIVIRQGKVARLESSLIPHEAQIEDLIF----LRKALNRADIPFLFIRNHKNRPV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNTTEP---TKKSE-KQLECLLT-HCIKVPMLVLDPALPANITLKDVPSLYPSFHSASDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNVAKPKNPSTNVSVVVFDST-----KDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 RLYRRRIAPGGFRFGSRFGVELQFWS----FEET-LIRCPVENSLTRKVLPRK---EVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DE-DISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLNLDNPRVTIVTHQDV
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4.7%; Score 228.5; DB 2; Length 373;
Best Local Similarity 31.3%; Pred. No. 9.4e-07;
Matches 52; Conservative 36; Mismatches 61; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 255.5; DB 2;
; Pred. No. 3.4e-08;
68; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Conservative
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Best Local Similarity
Matches 94; Conserv
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529 GFDAGDCGQDHFHELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNPIIRH 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907 WNALLLIGAGCLIVMVVLMLGALPGNRTRKRRMINASVWMPPMENEKNRRNHQSITSSQ 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759 NDSLVAPQEKQV------HKSILPNSLGVSE-------RLQRLTFPAVSVKVNG 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               800 HDQGQNPPLDLETTARFRVE----THTQKT---IGGNVTKEKPPSLIVPLESQMTKEKKI 852
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C,Species: Rattus norvegicus (Norway rat)
C,Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----MNSQHAKIKNQAIITDET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 CAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNS---GGSRYIAGGGGTGSIGVGHPWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688 FANGY -----CNQACNNEECLYDGMDCLPAVVRCPVKIREHCASRFANGICDPECNTNGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SWLADKFCDQACNVLSC
C,Accession: S18188
R;Weinmaster, G;Roberts, V.J.; Lemke, G.
Bevelopment 113, 199-205, 1991
A;Title: A homolog of Drosophila Notch expressed during mammalian de A;Title: A homology of Drosophila Notch expressed during mammalian de A;Reference number: S18188; MUID:92111383; PMID:1764995
A;Accession: S18188
A;Molecule type: mRNA
A;Residues: 1-2531 «WEI>
A;Coss-references: EMBL:X57405; NID:957634; PID:957635
A;Coss-references: EMBL:X57405; NID:957634; PID:957635
F;987-1018/Domain: EGF homology < EGF!>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589 ASIANKWKTIHLIMHSGMNATTI-HFNLTFQNTNDEEFK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
3.4%; Score 166.5; DB 2;
Best Local Similarity 20.4%; Pred. No. 0.058;
Matches 113; Conservative 43; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743 GFDGGDC-------DNET--
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                                                                                                                                                                                   RESULT 9
A49128
ccll-fate determining gene Notch2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A49128
R;Weinmaster, G; Roberts, V.J.; Lemke, G.
B;Velopment 116, 931-941, 1992
A;Title: Notch2: a second mammalian Notch gene.
A;Reference number: A49128; WUID:9312015; PMID:1295745
A;Reference number: A49128
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A/Accessioni, Ay9128
A/Accessioni, Ay9128
A/Scatus: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Accessioni Surversioni Schwann cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1404 PPFWGSHCESYTAPISTPPATCLSQYCADKARDGICDBACNSHACQWDGGDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 SWLADKF----CDQACNVLSCGFDAGDCGQDHFHELYK----VILLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4%; Score 168.5; DB 2; 26.2%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 YIAGGGGTGSIGVGHPW-QFGGGINSVSYCNQGC----
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                                                                     --GASLSAQTD 1781
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Best Local Similarity
Matches 44; Conserva
                                                                     1773
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A)Cross-references: BNBL:X66278; NID:g287987; FIDN:CAA48339.1; FID:g287988
A)Experimental source: embryo
A)Abote: sequence extracted from NCBI backbone (NCBIP:126159)
B;Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinat A;Reference number: A46438; MUID:9352998; PMID:8486742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Status: preliminary
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: nucleic acid
A;Molecule type: 1867-1932, "R,'1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',205
A;Molecule type: mbryo
A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betw
                                                                                          coexpressed in a wide variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1554
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Pred. No. 0.23;
3; Mismatches 204; Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           romosome 2
ankyrin repeat homology; EGF
                      R.Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A.Title: Motch A and Motch B--two mouse Notch homologues
A.Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown A;Nolecule type: mRNA A;Nolecule type: mRNA A;Residues: 1161-1547 < LAR>
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F,1063-1094/Domain: EGF homology «EG16»
F,1149-1180/Domain: EGF homology «EG17»
F,1187-1218/Domain: EGF homology «EG18»
F,1233-1264/Domain: EGF homology «EG18»
F,1352-1383/Domain: EGF homology «EGF4»
F,1351-1425/Domain: EGF homology «EGF4»
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Best Local Similarity 20.4%
Matches 119; Conservative
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A,Note: proximal region of
C,Superfamily: Notch protei
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F;607-638/Domain: EGF hr
F;627-788/Domain: EGF hr
F;777-788/Domain: EGF hr
F;775-94/Domain: EGF hr
F;911-942/Domain: EGF hr
F;911-942/Domain: EGF hr
F;911-942/Domain: EGF hr
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F;1025-1056/Domain:
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F;2016-2048/Domain:
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Asstatus: not compared with conceptual translation
Associate type: nucleic acid
Associates: 1-2531 - 5E1.
Associates: 1-2531 - 5E1.
Associates: 1-2531 - 5E1.
Associated: 1-253
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C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A46019; 822144; C49175; B46438; P46438; PHI569; S32109
B;Gel Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; G
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of A;Accession: A46019; MUID:93194170; PMID:8449489
                                                                                                                                                                                                                                                                                             27;
                                                                                                                                                                                                                                                                                                                                                                                                     GRDIPP------PQIEEACELPECQEDAGNK-----VCNLQCNNHACGWDGGDCSLN 1482
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1692 FLGALASLGSLNIPYKIBAV-KSETVEPPLPSQLHLMYVAAAAFVLLFFVGCGVLLSRKR 1750
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                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                      Score 165, DB 2; Length 2531;
Pred. No. 0.17;
4; Mismatches 178; Indels 18
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A;Molecule type: mRNA
A;Residues: 1551-2108,'Q',2110-2114,'ALP',2118-2170 <FRA>
F;1233-1264/Domain: EGF homology <EGF2>
F;1917-1949/Domain: ankyrin repeat homology <AN1>
F;1950-1982/Domain: ankyrin repeat homology <AN2>
F;1964-2016/Domain: ankyrin repeat homology <AN3>
F;2017-2049/Domain: ankyrin repeat homology <AN3>
F;2017-2049/Domain: ankyrin repeat homology <AN4>
F;2050-2082/Domain: ankyrin repeat homology <AN5>
                                                                                                                                                                                                                                                                                    64;
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Best Local Similarity
Matches 111; Conserv
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HAN	
Db 1555 EWDGLDCA-EHVPERLAAGTLVLVVLLPPDQLRNNSPHFLRELSHVLHTNVVFKRDA 1610  Qy 577 EGAYSDNPIIRHASIANKWKTIHLIMHSGWNATTIHFNLTFQNT 620	RESULT 13 824612 12412 12502012 12502012 12502012 12502012 1260201

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Discribe: Mus musculus (house mouse)
()Species: Mus musculus (house mouse)
()Species: Mus musculus (house mouse)
()Accession: 109059
()Accession: T09059
()Accession: T09059
()Accession: T09059
()Accession: L.) Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc submitted to the EMBL Data Library, October 1997
()Accession: Sequence of the mouse major histocompatibility locus class III region.
()A;Reference number: 216543
()A;Accession: T09059
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A;Nap position: 17
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
A;Introns: 22/1; 1761/3
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Keywords: receptor; signal transduction
F;514-545/Domain: EGF homology < EGF>
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         9
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                                                433 WPVPNC-----AEGCPGSWIK----DGYCDKACNNSACDWDGGDCSGNSGGSRY 477
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A;Molecule type: DNA
A;Residues: 1-1964 <ROW>
A;Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947
      Gaps
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      65;
                                                                                                         1367 WIGPRCEAPAAPEVSEEPRCPRAACQAKRGDORCDRECNSPGCGWDGGDC
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3.1%; Score 152; DB 2; Length 1964;
Best Local Similarity 28.1%; Pred. No. 0.76;
Matches 41; Conservative 11; Mismatches 32; Indels 62
38; Conservative 14; Mismatches 37; Indels
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mycobacteri actinobacil actinobacil

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4907
1 MLFKLLQRQTYTCLSHRYGL.....SLKTQLAYFTDSKNTGRQLK
  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                       - protein search, using sw model
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## ALIGNMENTS

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

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Scoring table:

Searched:

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base		UniPro 1: uni 2: uni	<pre>UniProt_02:* !: uniprot_sprot:* ?: uniprot_trembl:*</pre>	# Bpro trem	tt:* lb1:*			
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		o <del>k</del> e			SUMMARIES		R RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
1.	Score	ery	Length	DB	QI	Description	ra ra	Muzakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., Omura Y.,
н 0		91.2	847	77.0	096N13	Q96n13 homo sapien	R R	Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
(4)	565.5	523	921	1010	Q699R5		<b>\$ \$</b>	Tanal H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
٠,	2495	50.3	490	N (N	AAH60638 Q6IPWS	Aah60638 mus muscu O6ipw5 homo sapien	ዲ	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
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	734.5	15.0	3000	101	061340	V 0	8 8	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Shziki O.
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	486.5 360	o r o w	717		Q7Q098 Q9BUAS		RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
	329	6.7	602		091112	) (V	¥ \$	rujimori I., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
	322.5	 	9, 70 4, 80 1, 60 1, 70		Q9L114 069853	Q911i4 streptomyce O69853 streptomyce	RA RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R. Kawakami T. Nomochi S. 1104 F. Okitani R. Kawakami T. Nomochi S.
	320.5	ิ กับ	486 1486		Q7X4S1	[ ]	RA:	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
	287		238		QSGPD3	Obygai streptomyce Q8gpd3 streptococc	¥ ¥	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sudano T., Satoh T., Shirai V., Takahashi V., Makadana Y
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	266 266	ሊ ቤ 4. 4	545	00	Q84D00	00	RT	Nakal N., Iada I., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human
	200	. 4.	545		068215	OSB215 neisseria m	RT	CDNAB.";
	260.5	ю G	442		Q86IW6		a B B B	Mat. Genet. 50:40-49 (2004). EMBL; AKO56137; BAB71102.1;
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	256.5	101	364	10	271403 AAQ12659	V/14u9 naemopnilus Aaq12659 haemophil	<u>к</u> с	InterPro; IPR000800; Notch region. Pfam: PF06464; DMAP binding: 1.
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Result No.

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61 ACKSFQNRLCLPMPIDVVYTWVNGTDLBLLKBLQQVREQMBEBQKAMREILGKNTTEPFK 120
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307 SAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLNLDNPRVT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYSHSKG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 NATTIHFNLTFONTNDEEFKMQITVEVDTREGPKLNSTAQKGYENLVSPITLLPEAEILF 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 IVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYSHSKG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCSGNSGGSRYIAGGGGTGS 486
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                                                                                                                                                                                                                                                                                                                                                                                                    AND TASSUES AND THE COMPLETE SEQUENCES OF Unidentified human genes. XV.

The complete sequences of 100 new cDNA clones from brain which code

IT he complete sequences of 100 new cDNA clones from brain which code

IT he complete sequences of 100 new cDNA clones from brain which code

IT he sequences of 137-145 (1999).

BENBL, AB033034; BAA86522.2.

BENBL, AB033034; BAA86522.2.

ROJ GO:0016020; C:membrane; IEA.

ROJ GO:0016020; C:membrane; IEA.

ROJ GO:0016020; F:call differentiation; IEA.

ROJ GO:0016020; F:call differentiation; IEA.

RICEPPO: IPRO1056; DNAP binding.

RICEPPO: IPRO1056; Notch region.

REAM: PFC06464; DNAP binding; 1.

REAM: PFC0666; Notch; 1.

REAM: PRO0066; Notch; 1.

REAM: PRO0066; Notch; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    Last sequence update)
Last annotation update)
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99.8%; Pred. No. 1.9e-197;
ive 0; Mismatches 1;
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01-OCT-2002 (TrEMBLrel. 22, L
01-MAR-2004 (TrEMBLrel. 26, L
KIAA1208 protein (Fragment).
Name=KIAA1208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621; Conservative
                                                                                                                                                         Homo sapiens (Human).
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847 TKEKKITGKEKENSRMEENAENHIGVTEVLLGRKLQHYTDSYLGFLPWEKKKYFQDLLDE 906

950 AA.

Q9ULL2 PRELIMINARY; PRT; Q9ULL2; 1reMaY-2000 (TrEMBLrel. 13, Created)

RESULT 2 Q9ULL2 406

466 360 526 586

240

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FIVTNGQIPSWLNLDNPRVTIVTHQDIFQNLSHLPTFSSPAIESHIHRIEGLSQXFIYLN 300
587 RHASIANKWKTIHLIMHSGMNATTIHFNLTFQNTNDEEFKMQITVEVDTREGPKLNSTAQ 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           707 AQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQ 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 GVIVSKEMLSPLIVPPESHLP-----KEEESDRAEGNA---VPVKELVPGRRLQ---Q
                                                                                                                                                                                                                                                                                                                                               SCGFDAGDCGQDHFHELYKVILLPNQTHYIIPKGECLPYFSFAEVAKRGVEGAYSDNFII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 KGYENLVSPITLLPEAEILFEDIPKEKRFPKFKRHDVNSTRRAQEEVKIPLVNISLLPKD
                                                                                        NMTIDGKELTISPAYLLWDLSAISOSKQDEDVSASRFEDNEELRYSLRSIERHAPWVRNI
                                                                                                                            FIVTNGQIPSWLNLDNPRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLN
                                                                                                                                                                                                                                                                         DCSGNSGGSRYIAGGGGTGSIGVGHPWQFGGGINSVSYCNQGCANSWLADKFCDQACNVL
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                                                                                                                                                                                                                         DDVMFGKDVWPDDFYSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 EKQVHKSILPNSLGVSERLQRLTFPAVSVKVNGHDQGQNPPLDLETTARFRVETHTQKTI
                                                        NMTIDGKELTISPAYLLWDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRNI
                                                                                                                                                                                                   DDVMFGKDVWPDDFYSHSKGQKVYLTWPVPNCAEGCPGSWIKDGYCDKACNNSACDWDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6; TISSUE=Brain;
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=2238257; PubMed=1247932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                  887 SYLGFLPWEKKKYFQDLLDBEESLKTQLAYFTDSKNTGRQLK 928
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Last annotation update)
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Mus musculus (Mouse).
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AAH60638;
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STAIN-C57BJ/6; TISSUB-Brain;

MEDLINE-238825; DubMed-1247932;

Altschul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Babat N.K.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Babat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Boask S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunzarte P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rachy J., Helton B.K., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
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MREILGKNTTEPTKKSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASD 166
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Sciurognathi, Muridae, Murinae, Mus.
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC060638, AAH60638.1;
InterPro; IPR010948; BF-hand
InterPro; IPR010983; EF_Hand like.
InterPro; IPR00800; Notch_region.
Pfam; PF00066; efhand; 1.
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Hypothetical protein.
SEQUENCE 921 AA; 104970 MW; 12879CDE978D87BB CRC64;
                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                921 AA
                                                   EESLKTQLAYFTDSKNTGRQLK 928
                                                                           PRT;
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Mammalia; Butheria; Rodentia;
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 61.4%;
Matches 505; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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MEDLINE=22388257; PubMed=12477932;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
MGC4170 protein.
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                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 AQLSLNTLDLQLEHGDITLKGYNLSKSALLRSFLMNSQHAKIKNQAIITDETNDSLVAPQ
                                                                                                                                                                                                                                                                                                 107 MREILGKNTTEPTKKSEKQLECLLTHCIKVPMLVLDPALPANITLKDVPSLYPSFHSASD
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                                                                                                                                                                             Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                 EMBL, BC066638, AAH60638.1, -.
Hypothetical protein.
SEQUENCE 921 AA; 104970 MW; 12879CDB978D87BB CRC64;
                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                              Local Similarity 61.4%;
les 505; Conservative
                                                                                                                 and mouse cDNA sequences.";
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,
Batchul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A.N., Gabs E.S.,
Norland A., Young A.C., Shevohenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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9
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo
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Strausberg R.;
Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL; BC071887; AAH71887.1; -.
InterPro; IRR000800; Notch_region.
Pfam; PF00066; Notch; 1.
SWART; SM00004; NL; 1.
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                                                                                                          887 SYLGFLPWEKKKYFQDLLDEEESLKTQLAYFTDSKNTGRQLK
                                                                                                                                                                  552 NYPGFLPWEKKKYFQDLLDEEESLKTQLAYFTDSKHTGRQLK
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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KSEKQLECLITHCIKVPMLVLDPALPANITLKDLPSLYPSFHSASDIFNVAKPKNPSTNV 180
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                                                 61 AGKSFQNRLCLPMPIDVVYIWVNGTDLELLKELQQVREQMEEEQKAMREILGKUYTEPTK
                                                                                                                                                                                                                                                                                       SVVVFDSTKDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPTFKET
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to v-maf musculoaponeurotic fibrosarcoma oncogene family,
protein B (Avian) (Fragment).
Endersypta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Hono.
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TISSUELiver;
Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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100.0%; Pred. No. 1.3e-43;
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GO; GO:005509; F:calcium ion binding; IER
InterPro; IPR010509; E:calcium ion binding;
InterPro; IPR002048; EF-hand
InterPro; IPR002048; EF-hand
InterPro; IPR003083; EF-hand like.
Pfam; PF06464; DMAP binding; 1.
PR0541E; PS00036; efhand; 1.
PR0541E; PS00038; EF-HAND; UNKNOWN 1.
SEQÜENCE 490 AA; 57411 MW; 37B19FE0D12
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Best Local Similarity 100.
Matches 162; Conservative
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WE MEDIINE 22388257; PubMed=12477932;

WE MEDIINE 22388257; PubMed=12477932;

A Strausberg N.L. Felingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Usdain T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rahards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rahards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rahards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rhilaton D.K., Muzny D.M., Sodergren B.J., Iu. X., Gibbs R.A.,

Whilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhy Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhy Mrithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhy Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Khyannski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Rhy Generation and initial analysis of more than 15,000 full-length human muse coby series and series an
SVVVPDSTXDVEDAHSGLLKGNSRQTVWRGYLTTDKEVPGLVLMQDLAFLSGFPPTFKET 240
                                                                                                                              NQLKTKLPENLSSKVKLIQLYSEASVALLKLNNPKDFQELNKQTKKNMT1DGKELT1SPA 300
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordes S.P., Barsh G.S., The modes a novel basic domain-leucine ripper transcription factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
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                                                                                                                                                                                                          Last sequence update)
Last annotation update)
transcription factor (Fragment).
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es 71; Indels
                                                                                     384 AA.
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                                                                                                                                                                           Created)
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                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01,
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Matches 165; Conservative
                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Created) Last sequence update) Last annotation update)

(TrEMBLrel. 13, (TrEMBLrel. 24, (TrEMBLrel. 26,

01-MAY-2000 ( 01-JUN-2003 ( 01-MAR-2004 (

Q9V553; Q9V553

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PREDENCE FOR N.A.

RAMEDINE-20196006; PubMed=10711132,

RADRINE-20196006; RADRINE-20
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MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.W., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Storated S., Sodergren B.J., Suinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstong a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDDINE-22426070; PubMed=12537573; Kaminker J.S. Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fisles E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Calniker S.E., *Ashburner M., Calniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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RANGER REPRESENTATION OF STANTARY SERVICES OF STANT
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Gaps

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Length 666;

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315 DEDISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLNLDNPRVTIVTHQDVF 374
                                                                                                                                                                         DDKYDPSRFDDKNELRYSLRSLEKHAAWIRHVYIVTNGQIPSWLDLSYERVTVVPHEVLA 145
                                                                                                                                                                                                                                              146 PDPDQLPTFSSSAIETFLHRIPKLSKRFLYLNDDIFLGAPLYPEDLYTEAEGVRVYQAWM 205
                                                                                                                                                                                                                   RNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDVMFGKDVWPDDFYSHSKGQKVYLTWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 SPAYLLWDLSAISOSKODEDISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 DDLQTLAEGVKVFTAWIVPDCAPDCPWMFVGDGSCDRDCFLEECQFDGGDCDHPDYGADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera; Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
           F6FDB6D1C1C39248 CRC64;
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Name=agCG49111; ORFNames=ENSANGG00000017588;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                              VPGCALDCPWTYIGDGACDRHCNIDACQFDGGDCS 240
                                                     Score 488; DB 2;
Pred. No. 1.1e-21;
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Pred. No. 1.6e-21;
                                                                                                                                                                                                                                                                                                        VPNCAEGCPGSWIKDGYCDKACNNSACDWDGGDCS
                                                                       54.2%; Pred. No. 1.1e
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           77745 MW;
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                                                                       L Similarity 54.2% 84; Conservative
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           666 AA;
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01-JUN-2001 (
01-OCT-2002 (
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Best Local S:
Matches 84
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Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.B., de Grey A.D., Drygdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Berkeley;
Stapteton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                        Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Indels
                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003834; AAF58967.2; -.
IntAct; Q9V553; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AX089618; AAL90356.1; -. Flymase; FEMRO03392; CG8027.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
InterPro; IFR00800; Notch_region.
PF00066; Notch; 1.
                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77731 MW; EA232EC57C754FF6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 VPGCALDCPWTYIGDGACDRHCNIDACQFDGGDCS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.9%; Score 488; DB 2;
                                                                                                                                                  systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                 FIYBase, FBGN003392; Ccc...
GO, GO:0016020; C:membrane; IEA.
GO; GO:0030154; P:cell differentiation; IEA.
InterPro; IPR00800; Notch_region.
Pfam; PF00066; Notch; 1.
sROUENCE 666 AA; 77731 MW; EA232EC57C75
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
RESS039.
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hes 84; Conservative
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                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
Hopwood D.A.,
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Best Local Similarity 33.6%;
Marches 79; Conservative 4
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Best Local Similarity
Matches 93; Conserv
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Q9L1I4
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                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jezeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rickingez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Salska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLFKLLQRQTYTCLSHRYGLYVCFLGVVVTIVSAFQFGEVVLBWSRDQYHVLFDSYRDNI
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MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
Bettley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-WAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein SCO2594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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NCBI_TaxID=1902;
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100.0%; Pred. No. 3.6e-15;
ive 0; Mismatches 0;
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68; Conservative
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                             WGC4170 protein
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01-OCT-2000
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Best Local 8
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Q9L112
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                                                                                                                                                                                                                                                                                                                 :||::||||||||::|
297 VDGSD----PAWIRSRAEFSDRPYHEEAANAARYLSRDELRYSLRSINLYAPWVRNIYLV
                                                                                                                                                                                                                                                                                                                                                                                                                  290 IDGKELTISPAYLLMDLSAISQSKQDEDISASRFEDNEELRYSLRSIERHAPWVRNIFIV
                                                                                                                                                                                                                                                                                                                                                                                       350 INGQIPSWLNLDNPRVTIVTHQDVFRNLSHLPTFSSPAIESHIHRIEGLSQKFIYLNDDV
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 RKMKHVPHALHRGVLEAIETDFADEHRRTAASRFRSAGDISVTSSLHHYVAFHTG 527
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417.147.147(2002).

Nature 417.141.147(2002).

Complete proteome; Hypothetical protein.

SEQUENCE 602 AA; 67501 MW; 720EAB86A31D943F CRC64;
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Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                            6.7%; Score 329; DB 2; Length 602; 3.6%; Pred. No. 7.7e-12; ve 44; Mismatches 82; Indels 3
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EMBL; AL939113; CAB75373.1; -.

EXCONOBERGES: P: biosynthesis; IEA.

InterPro; IPR001296; Glyco_trans_1.

Pfam; PF00534; Glyco_trans_1.

Complete proceome; Transferase.

EXEQUENCE 942 AA; 105062 MW; 108B737B98A97B80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=SCO2592; ORFNames=SCC88.03c;
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605
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                                                                                                                                                                                                                                             662 AESSGDE---AARFRNRDELRYSLASLAMFAPWIRKIYLVTDDGTPEWLNTEHEGIEVVS 718
| | :: | : | : | : | : | 490 NPRRRIAVDAAEQTR-VRKALAGAYEG---KAVYAELLKPRTHAPGVLLAERLEAVGEVA 545
                                                        229 FLSGFPPTFKETNOLK-----TKLPENLSSK------VKLLQLYSE 263
                                                                                                                                          -LSAI 309
                                                                                                                                                                                                                                                                                               370 HODVERNISHLPTESSPALESHIHRIEGISQKFIYLNDDVMFGKDVWPDDFYSHSKGQKV 429
                                                                                                                                                                                                                                                                                                                                         778
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282 VDGND----PA---WRRRRSAYDGGYHAESANAARYISRDELRYSLRALEQNAPWVRHVH 334
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                                                                                            546 GLRVFRPVVTSTRTLRFGPAYGCDIEFWROVPEBEGGDGOFVAPLRPSAVGPKLPSLTPD
                                                                                                                                                                     606 ARTRV----KDREYPTLEPLTRKLVSDITFPVDAVYTWVDDSDPRWCERRARRAALGLE
                                                                                                                                                                                                                   310 SQSKODEDISASRFEDNEELRYSLRSIERHAPWVRNIFIVTNGQIPSWLNLDNPRVTIVT
                                                                                                                                                                                                                                                                                                                        Gaps
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STRAIN=A3(2) / M145.
MEDLINE=21996410, PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410, PubMed=12000953; DOI=10.1038/417141a;
MEDLINE=21996410, PubMed=12000953; DOI=10.1038/417141a;
Thomson N.R., Janes K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBI; A1939126; CA119235.1; --
PIR; T34703; T34703.
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6.6%; Score 322.5; DB 2; Length 586;
Best Local Similarity 46.3%; Pred. No. 1.9e-11;
Matches 62; Conservative 30; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                      ASVALLKINNPKDFQELNKQTKK-----NMTIDGKELTISPAYLLWD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Hypothetical protein.
SEQUENCE 586 AA; 66009 MW; 75F98F0916484116 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SCO6023.
OrderedousNames=SCO6023, ORFNames=SCIC3.11;
Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                        430 YLTWPVPNCAEGCPGSWIKDGYCDKACNNSA 460
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Search completed: November 21, 2004, 13:02:00 Job time : 135.057 secs

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November 21, 2004, 12:38:18; Search time 37.6766 Seconds (without alignments) 3122.980 Million cell updates/sec
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1731
1 DTFADSLRYVNKILMSKFGF......RKIFPRRRIHKEASPNRIRV 328
                                                                                                                                                                                                                                                                                                                                                           2002273
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                 2002273 seqs, 358729299 residues
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseq11986s: geneseq1200s: geneseq200s: geneseq2002s: geneseq2002s: geneseq2003s: geneseq2003s: A Geneseq 23Sep04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	6	Query	1	í	4	
. !	score	Match	Length	DB.	ID	Description
	1731	100.0	328	4	ABR61377	Abr61377 Human Glc
a	1731	100.0	328	7	ADD27813	m
~	1731	100.0	328	7	ABW01489	Human
44	1731	100.0	328	7	ABW01538	
'n	1731	100.0	1196	'n	AAE25294	Human
9	1731	100.0	1256	Ŋ	AAE25290	Human
7	1698	98.1	328	4	ABR61380	Murine
œ	1698	98.1	328	7	ADD27818	GlcNAc-
σ	1698	98.1	328	۲	ABW01492	
10	1698	98.1	328	7	ABW01541	Mouse
-	1487	85.9	1199	7	ADD27810	Solubl
C)	1487	85.9	1199	۲	ABW01487	
m	1487	85.9	1199	7	ABW01536	
41	1276	73.7	248	7	ADG39858	
ın	1140	62.9	663	7	ADG39855	Protein
w	1140	62.9	1459	9	ABU07381	Human pr
_	1140	62.9	1459	7	ADG39794	Human
œ	704	40.7	132	4	AAB93369	Aab93369 Human pro
o.	581	33.6	384	7	ADG39857	
0	206	29.5	652	4	ABB59094	Abb59094 Drosophil
_	495.5	28,6	651	^	ADG39859	
C)	402	23.2	502	4	ABR61383	Partial
<u>~</u>	402	23.2	502	7	ADD27824	Fruit
	402		502	7	ABW01495	
	402	23.2	502	^	ABW01544	Partia

	Abo57141 Human qen	Abr61390 Bovine Gl		_			Adk63602 Disease t	_	_							Aar79331 IL-3 cont		_	_	Aael3988 Myelopoie
	ABO57141	ABR61390	AAB68261	AAM88395	ABB77984	ABR53887	ADK63602	AAW79296	ADD27834	ABP26069	ABB49330	ABG06505	ADQ17932	AAM40883	AAR79314	AAR79331	AAY53212	AAY53195	AAE14006	AAE13988
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(	7.6	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESU	RESULT 1
ABRE	
23	ABR61377 standard; protein; 328 AA.
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¥	Abro1377;
{ E	OF TATE - DOOD (6) was contained
Z X	76111
E C	Himan GleNAc-phoephotraneferace beta-enbrinit
X	
Š	Human; N-acetylglucosamine-1-phosphotransferase; nephrotropic;
Ž	GlcNAc-phosphotranferase; phosphodiester alpha-GlcNAcase;
Σ	N-acetylglucosamine-1-phosphodiester alpha-N-Acetylglucosaminidase;
<b>3</b> §	
X X	lysosomal storage disease; enzyme; beta-subunit.
Ö	Homo ganjens
×	
PN	US6537785-B1,
×	
PD	25-MAR-2003.
X	
PF	10-AUG-2000; 2000US-00636077.
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PR	14-SEP-1999; 99US-0153831P.
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PA	(GENZ-) GENZYME GLYCOBIOLOGY RES INST INC.
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ž X	N-FSDD; ACCBIOOI.
F	Novel N-acety a ncosamine-1-phosphotransferase and N-acety a ncosamine-1-
Ā	and in according to the results of
i E	
PT	Thungsoft Surpage to contact to the contact to
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PS	Disclosure; Page 28-29; 62pp; English.
X	
ខ្ល	The invention relates to a novel isolated human N-acetylglucosamine-1-
S	phosphotransferase (GlcNAc-phosphotranferase) (I) and phosphodiester
ខ្ព	alpha-GlcNAcase (N-acetylglucosamine-1-phosphodiester alpha-N-
ខ	
႘	nephrotropic activity, and may be useful in enzyme replacement therapy. A
႘	protein of the invention (I), (II) is useful for preparing a
ပ ပ	phosphorylated lysosomal hydrolase. The phosphorylated hydrolase
ပ္ပ	comprising a terminal mannose-6-phosphate, is useful for treating a

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acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease. The present sequence represents the amino acid sequence of the human GlcNAc-phosphotransferase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS2003124652-A1.
                                                                                         Sequence 328 AA;
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          present sequence
                                                                                                                                                                                         DIPADSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS
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                                                                                                                             Gaps
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UDP-N-acetylglucosamine; lysosomal storage disease; Fabry's disease.
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                                                                                          Length 328;
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          suffering from a lysosomal storage disease. The in the exemplification of the invention
                                                                                            100.0%; Score 1731; DB 4;
100.0%; Pred. No. 7.3e-160;
ive 0; Mismatches 0;
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                                                                                                                               Conservative
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N-PSDB; ADD27811.
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                                                                                                              Similarity
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                                                              Sequence 328 AA;
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                                                                                                                                 Matches 328;
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The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble  $\operatorname{GlcNAc}$ -phosphotransferase (UDP-N-

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                                                                                                                                                              61 EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
                                                                                                                                                                                             GLEHMLINCSKMLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK
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                                                                                           1 DTFADSLRYVVKILNSKFGFTSRKVPAHMPHMIDRIVMQSLQDMFPEEFDKTSFHKVRHS
                                                                                                                                  61 BDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDRBIRTLATRIHELPLSLQDLT
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                                   Gaps
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 Length 328;
                                   Indels
100.0%; Score 1731; DB 7;
100.0%; Pred. No. 7.3e-160;
ive 0; Mismatches 0;
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   Query Match
Best Local Similarity 100.
Matches 328; Conservative
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N-PSDB; AAD62491.
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N-PSDB; AAD62650.

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         The invention relates to a method for producing a high mannose glycoprotein. The method comprises: introducing and expressing a polynucleotide encoding a glycoprotein into a mammalian cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of deoxymannojirimycin and kifunensine to inhibit glycopylation of the glycoprotein; and collecting the glycoprotein. The invention is useful gene therapy. The method is useful for producing a high mannose glycoprotein in a complex carbohydrate deficient cell for treating lysosomal storage disease. The present sequence is human N-acetylglucosamine-1 (GlcNAc)-phosphotransferase beta subunit precursor
                                                                                                                                                                                                                                                                                                                                                       EDMOFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
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100.0%; Pred. No. 7.3e-160;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                 Matches 328; Conservative
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                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                        Sequence 328 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           having reduced complex carbohydrates by culturing the lectin resistant having reduced complex carbohydrates by culturing the lectin resistant ammunalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is human N-acetylglucosamine-1 (GlcNAc)-phosphotransferase beta subunit precursor protein
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                                 Producing a glycoprotein with reduced complex carbohydrates by culting the lectin resistant mammalian cell expressing the glycoprotein for treating lysosomal storage disease.
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                                                                                                                                                                                                                                                                                                                     Length 328;
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/note= "Cytosolic domain"
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/label= Signal_peptide
1. .19
                                                                                                      Claim 10; Page 18-19; 46pp; English
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Human; nucleic acid-associated protein; NAAP-9; neurological disorder; arteriosclerosis; cancer; cell proliferative disorder; atherosclerosis; lymphoma; epilepsy; Alzheimer's disease; developmental; anticonvulsant; autoimmune disorder; AlDS; allergy; anaemia; stroke; malaria; leishmania; gene therapy; nootropic; neuroprotective; cerebroprotective; virucide; immunosuppressive; protozoacide; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid associated proteins and nucleic acids for diagnosing, treating and preventing cell proliferative (e.g. cancers), neurological (e.g. epilepsy or stroke) or autoimmune disorders (e.g. AIDS).
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241 RDFYESMFPIPSQFELPREYRNRFLHWHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFF
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H, Batra S, Ding L, Lal PG;
AR, Griffin JA, Xu Y, Azimzal Y;
BH, Mason PM, Burford N, Hafalia;
Emerling BM, Marquis JP, Lee SY;
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/note= "Notch domain"
500. .536
1016= "Notch domain"
1018. .1030
/note= "EF-hand calcium-binding domain"
                                                                                                                                                                                                                                                                     Human nucleic acid-associated protein (NAAP-9).
                                                                                    AEQLIALKRKIFPRRRIHKEASPNRIRV 1196
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                                                                  301 AEQLIALKRKIFPRRRIHKEASPNRIRV
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                                                                                                                                                                             AAE25290 standard; protein; 1256
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05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262302P.
23-JAN-2001; 2001US-0263823P.
02-FFB-2001; 2001US-0266088P.
29-OCT-2001; 2001US-0346442P.
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Walia NK, Tribouley KW, Yue
Borowsky ML, Lu DAM, Gandhi
Gjetzen KJ, Tang YI, Warren
Gietzen KA, Yang J, Gorvad AE,
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N-PSDB; AAD41199.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to nucleic acid-associated proteins (NAAP) and nucleic acids. The nucleic acid and amino acid sequences are useful for diagnosing, treating and preventing cell proliferative e.g. arteriosclerosis, lymphoma or cancers), neurological (e.g. epilepsy, Alzheimer's disease or stroke), developmental, and autoimmune disorders (e.g. AIDS, allergies, or anaemia) or infections (e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful in gene therapy. The present sequence is human NAAP-13
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H, Batra S, Ding L, Lal PG;
K, Griffin JA, Xu Y, Azimzai Y;
BA, Mason PM, Burford N, Hafalia AJA;
Emerling BM, Marquis JP, Lee SY;
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                        /note= "Mature human NAAP-13"
43. .1152
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                                                      /note= "Non-cytosolic domai
1153. 1175
/note= "Transmembrane domai
1176. 1196
/note= "Cytosolic domain"
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05-JAN-2001; 2001US-0260081P.
16-JAN-2001; 2001US-0262302P.
23-JAN-2001; 2001US-0263823P.
02-FBB-2001; 2001US-0266088P.
29-OCT-2001; 2001US-0348442P.
                                                                                                                                                                                                                   2001WO-US050256
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. A, Reddy R;
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N-PSDB; AAD41203.
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es 328; Conserv
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241 RDFYESMFPIPSQFELPREXRNRFLEMHELQEWRAYRDKLKFWTHCVLATLIIFTIFSFF 300
                                                 The invention relates to a novel isolated human N-acetylglucosamine-1-phosphortranferases (il.) and phosphoredieter alpha-discharases (id.) and phosphoredieter alpha-discharases (in.) and phosphodiester alpha-detylglucosaminidase) (II). The protein of the invention has rephrotropic activity, and may be useful in enzyme replacement therapy. A protein of the invention (I), is useful for preparing a phosphorylated lysosomal hydrolase. The phosphorylated hydrolase comprising a terminal mannose-6-phosphate, is useful for treating a patient suffering from a lysosomal storage disease. The present sequence is used in the exemplification of the invention
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UDP-N-acetylglucosamine; lysosomal storage disease; Fabry's disease;
                                                                                                                                                                                                                                                                                                Length 328;
                                                                                                                                                                                                                                                                                              Query Match 98.1%; Score 1698; DB 4; Length 3 Best Local Similarity 97.6%; Pred. No. 1.2e-156; Matches 320; Conservative 7; Mismatches 1; Indels
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                 Disclosure; Page 35-36; 62pp; English
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                                                                                                                                                                                                                                                            Sequence 328 AA;
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ADD27818
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                                                                                                                                                                                                                                         988
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(e.g. malaria, or leishmania), as well as in assessing the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of nucleic acid-associated proteins. The invention is useful gene therapy. The present sequence is human NAAP-9
                                                                                                                                                                                                                                                                                                      EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
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                                                                                                                              1256;
                                                                                                                              Length
                                                                                                                                                                  Indels
                                                                                                                          100.0%; Score 1731; DB 5;
100.0%; Pred. No. 5.1e-159;
ive 0; Mismatches 0;
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                                                                                                                                                                  328; Conservative
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N-PSDB; ACC81007.
                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                         98.1%;
llarity 97.6%;
Conservative
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                      WPI; 2003-810984/76.
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Matches 320; Conserv
                                                                                                                                                                                                                                                                                   Sequence 328 AA;
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Canfield
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                                                                                                The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble GlcNAc-phosphotransferase (UDP-N-acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease. The present sequence represents the amino acid sequence of a GlcNAc-phosphotransferase associated protein.
                                                                                                                                                                                                                                                                                                                        EDMOFAFSYFYYLMSAVQPLNISQVFDEVDIDQSGVLSDREIRTLATRIHELPLSLQDLT 120
                                                                                                                                                                                                                                                                                                                                         EDMOFAPSYFYYLMSAVOPLNISQVFHEVDTDQSGVLSDREIRTLATRIHDLPLSLQDLT 120
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         Phosphorylating a protein for treating a patient suffering from a
lysosomal storage disease e.g. Fabry's disease by contacting the protein
with a soluble GlcNAc-phosphotransferase and producing a phosphorylated
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                                                                                                                                                                                                                     Length 328;
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lysosomal storage disease; gastrointestinal; mouse;
lectin resistant cell; deoxymannojirimycin; kifunensine;
                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                    Score 1698; DB 7;
Pred. No. 1.2e-156;
                                                                                                                                                                                                                                              7; Mismatches
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                                                                           Disclosure; SEQ ID NO 10; 55pp; English.
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                                                                                                                                                                                                                                              Matches 320; Conservative
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                                                                                                                                                                                            Sequence 328 AA;
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The invention relates to a method for producing a high mannose glycoprotein. The method comprises: introducing and expressing a plycoprotein into a mammalian cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of decoymentojiriwyoin and kifunensine to inhibit glycosylation of the glycoprotein; and collecting the glycoprotein. The invention is useful in gene therapy. The method is useful for producing a high mannose lycoprotein in a complex carbohydrate deficient cell for treating lysosomal storage disease. The present sequence is mouse protein used to illustrate the method of the invention
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Producing a high mannose glycoprotein for treating lysosomal storage disease, comprises culturing the lectin resistant mammalian cell in t presence of deoxymannojirimycin and kifunensine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse protein #2 used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1698; DB 7;
Pred. No. 1.2e-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
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                                                                                                                                                             Disclosure; Page 25-26; 46pp; English.
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1039 GLEHMLINCSKMLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK 1098
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                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of phosphorylating a protein comprising contacting the protein with a soluble GlcNAc-phosphotransferase (UDP-N-acetylglucosamine) and producing a phosphorylated protein. The method is useful for treating a patient suffering from a lysosomal storage disease e.g. Fabry's disease. The present sequence represents the amino acid sequence of soluble human GlcNAc-phosphotransferase.
                                                                                                                                                                                                                                                Phosphorylating a protein for treating a patient suffering from a
lysosomal storage disease e.g. Fabry's disease by contacting the protein
with a soluble GlcNAc-phosphotransferase and producing a phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFADSLRYVNKILNSKFGFISRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1487; DB 7; I
Pred. No. 2.9e-135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.9%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 2; 55pp; English
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                                    21-DEC-2001; 2001US-00023888.
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Best Local Similarity 100.
Matches 281; Conservative
                                                                                                              (NOVA-) NOVAZYME PHARM
                                                                                                                                                   Canfield W, Kudo M;
                                                                                                                                                                                          WPI; 2003-801323/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1199 AA,
                                                                                                                                                                                                           N-PSDB; ADD27809
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                                                                           21-DEC-2001;
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  26-JUN-2003
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                                                                                                                                                                                                                                                                                                             protein.
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ABW01487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLEHMLINCSKWLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK 180
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                                                                                                                                                                                                                                                                                   The present invention provides a method of producing a glycoprotein having reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is mouse protein used to illustrate the method of the invention
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                                                                                                                                                                        culturing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DTFADSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; protein phosphorylation; soluble GlcNAc-phosphotransferase; UDP-N-acetylglucosamine; lysosomal storage disease; Fabry's disease.
                                                                                                                                                                  Producing a glycoprotein with reduced complex carbohydrates by c
the lectin resistant mammalian cell expressing the glycoprotein
treating lysosomal storage disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1698; DB 7;
Pred. No. 1.2e-156;
7; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soluble human GlcNAc-phosphotransferase.
                                                                                                                                                                                                                                              Disclosure; Page 25-26; 46pp; English
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                21-DEC-2001; 2001US-00023890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.1%;
                                                     PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.6
Matches 320; Conservative
                                                                                                                               WPI; 2003-810985/76.
                                                     (NOVA-) NOVAZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 328 AA;
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                                                                                          Canfield
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1099 NKYRFEIMGEEEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVL 1158
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                                                                                                                                                                                                                                                  Producing a glycoprotein with reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein for treating lysosomal storage disease.
                                                                                                                                                                                                                                                                                                                                                      The present invention provides a method of producing a glycoprotein having reduced complex carbohydrates by culturing the lectin resistant mammalian cell expressing the glycoprotein. The method is useful for producing a glycoprotein with reduced complex carbohydrates for treating lysosomal storage disease. The present invention is also useful in gene therapy. The present sequence is N-acetylglucosamine (GlcNAC)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; NOVX; cardiomyopathy; atherosclerosis; hypertension; congenital heart defect; pulmonary stenosis; scleroderms; obsity; metabolic disturbance; obesity; transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer; diabetes; metabolic discorder; heoplasm; adenocarcinoma; fertility; haemophilia; graft versus host disease; AlDS; bronchial asthma; Crohn's disease; multiple sclerosis; infectious disease; anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           919 DIFADSLRYVNKIINSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEBFDKTSFHKVRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
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                                                                                                                                                                                                                                                                                                                           Claim 8; Page 10-13; 46pp; English.
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                                                               21-DEC-2001; 2001US-00023890.
                                                                                                  21-DEC-2001; 2001US-00023890
                                                                                                                                     (NOVA-) NOVAZYME PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281; Conservative
                                                                                                                                                                                                        WPI; 2003-810985/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1199 AA;
                                                                                                                                                                                                                       N-PSDB; AAD62649.
US2003124653-A1
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                                                                                                                                                                       Canfield WM;
                                03-JUL-2003.
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                                                                                                                                                                                                                                                                                                                         The invention relates to a method for producing a high mannose glycoprotein. The method comprises: introducing and expressing a polymucleotide encoding a glycoprotein into a mammalian cell; culturing the cell in the presence of a lectin to obtain a lectin resistant cell; isolating the cell; culturing the cell in the presence of decoymannojirinycin and kitunensine to inhibit glycosylation of the glycoprotein, and collecting the glycoprotein. The invention is useful in gene therapy. The method is useful for producing a high mannose alycoprotein in a complex carbohydrate deficient cell for treating lysosomal storage disease. The present sequence is N-acetylglucosamine-1 (GICNAc)-phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDMQFARSYRYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKYRFEIMGEEEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                          Producing a high mannose glycoprotein for treating lysosomal storage disease, comprises culturing the lectin resistant mammalian cell in the presence of deoxymannojirimycin and kifunensine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.9%; Score 1487; DB 7; L
100.0%; Pred. No. 2.9e-135;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                Claim 8; Page 10-13; 46pp; English
                                  21-DEC-2001; 2001US-00023889
                                                                     21-DEC-2001; 2001US-00023889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.9%;
                                                                                                       (NOVA-) NOVAZYME PHARM INC.
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Local Similarity 100.0
hes 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1199 AA;
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                                                                                                                                          Canfield WM;
     03-JUL-2003
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Length 1199; 0; Indels

85.9%; Score 1487; DB 7; I 100.0%; Pred. No. 2.9e-135; iive 0; Mismatches 0;

120

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Unidentified

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neurodegenerative disorder, Alzheimer's disease, Parkinson's disease, immune disorder; haematopoietic disorder; dyslipidaėmia;
                                                                                                                                                                                               Topper JN,
Gunther E,
                                                                                                                                                    MALYANKAR U M.
WASSERMAN S M.
BDINGER S R.
SMITHSON G.
GUNTHER E.
KOMUVES L.
                                                                                                                    SHIMKETS R A. PADIGARU M.
                                                                                                                               KEKUDA R.
SPYTEK K A.
MEHRABAN F.
TOPPER J N.
                                                                                                                                                                                                                WPI; 2003-900671/82.
                                                                                                          CEA.
                                                                                                                                                                                                                                     obesity, prostate camultiple sclerosis.
                                                                                                                                                                                           Guo X,
          wasting disorder
                                US2003203843-A1.
                                                                               25-APR-2001; 2
03-MAY-2001; 2
16-MAY-2001; 2
14-SEP-2001; 2
                      Homo sapiens
                                                                     23-APR-2001;
24-APR-2001;
                                                                                                                                                                                          Pena CEA, Gu
Mehraban F,
Smithson G,
                                                                20-APR-2001;
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                                                                                                                GNO
                                           30-OCT-2003
                                                                                                                               (XEKU/)
(SPYT/)
(MEHR/)
(TOPP/)
(MALY/)
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(SHIM/)
(PADI/)
                                                                                                          (PENA/)
                                                                                                                                                                                (KOMU/)
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The invention relates to a new isolated polypeptide comprising an amino acid sequence selected from 17 fully defined human NOVX sequences (even SEQ ID NOS between Ab03970 and Ab039802), a mature form of the NOVX main acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue of NOVX. Also included are an isolated nucleic acid (NA) molecule (Comprising a nucleic acid sequence encoding a NOVX polypeptide above (Codd SEQ ID NOS between Ab039769 and Ab039801), a nucleic acid fragment of NOVX NA), a vector comprising NOVX NA, a cell comprising the vector, an antibody that immunospecifically binds to NOVX, a method of determining the presence or amount of NOVX or NOVX, a method for determining the activity of NOVX, a method of resolution to a modulating the activity of NOVX, a method of treating an agent that binds to NOVX, associated disorder, a method for screening for a modulator of a cotivity or of latency or predisposition to a NOVX-associated disorder, a method for determining the presence of or predisposition to a disease subject and a method of treating a pathological state in a mammal by administering NOVX or an antibody that binds to NOVX. The NOVX associated disorder. The NOVX polypeptides and nucleic acid or antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease or a NOVX-associated disorder. The NOVX polypeptides and nucleic acid or antibody or treating pathologies, diseases encoding them are useful for diagnosing or treating pathologies, diseases New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or Shimkets RA, Padigaru M, Kekuda R, Spytek KA; Tu, Malyankar UM, Wasserman SM, Edinger SR; Sr E, Komuves L; Disclosure; SEQ ID NO 90; 215pp; English. , 2001US-0285609P. ; 2001US-0285748P. ; 2001US-028628P. ; 2001US-0286292P. ; 2001US-0288334P. ; 2001US-0288334P. 11-APR-2002; 2002US-00120801

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                  atherosclerosis, hypertension, congenital heart defects, pulmonary stenoats, scleroderma, obesity, metabolic disturbances associated with obesity, transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm, adenocarcinoma, fertility, haemophilia, graft versus host disease, horonial asthma, Crohn's disease, multiple sclerosis, infectious disease, anorexia, neurodegenerative disorders (e.g. Alzhaimer's disease, reparkinson's disease), immune disorders, haematopoietic disorders, dyslipidaemias, and wasting disorders, haematopoietic disorders. The polypeptides can be used as immunogens to produce antibodies and as vaccines. The sequences may further be used in chromosome mapping, identifying individual from minute biological samples (tissue typing), and in forensic identification of a biological samples (tissue typing), and in forensic identification of a biological samples (tissue typing), sequence is a protein showing sequence similarity to a NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 VFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLTGLEHMLINCSKWLPADITQLNNIP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 PTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDKNKYRFEIMGEEEIAFKMIRTNVSH 124
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    including cardiomyopathy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 VFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLTGLEHMLINCSKWLPADITQLNNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 PTQESYYDPULPPVTKSLVTNCKPVTDKIHKAYKDKNKYRFBIMGEBEIAFKMIRINVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 VVGQLDDIRKNPRKFVCLNDNIDƏNHKDAQTVKAVLRDFYESMFPIFSQBELPREYRNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 LHWHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFFAEQLIALKRKIFPRRRIHKEASPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 LHWHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFFAEQLIALKRKIFPRRRIHKEASPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVLRDFYESMFPIPSQFELPREYRNRF
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                                                                                                                                                                                                                                                                                                                                                                                             73.7%; Score 1276; DB 7; Length 248; 99.2%; Pred. No. 1.1e-115; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder; haematopoietic disorder; dyslipidaemia;
conditions associated with NOVX sequences,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         242; Conservative
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23-APR-2001; 2001US-0285748P.
24-APR-2001; 2001US-0286668P.
25-APR-2001; 2001US-0286292P.
30-MAY-2001; 2001US-0283334P.
16-MAY-2001; 2001US-0291334P.
14-SEP-2001; 2001US-0322284P.
                                                              MALYANKAR U M.
WASSERMAN S M.
BDINGER S R.
SMITHSON G.
GUNTHER E.
KOMUVES L.
                                     SHIMKETS R A.
PADIGARU M.
KEKUDA R.
SPYTEK R A.
MEHRABAN F.
TOPPER J N.
                                                                                                             WPI; 2003-900671/82
                              PENA C E A.
                                                                                             Pena CEA,
                                                                           (SMIT/)
(GUNT/)
(KOMU/)
                              (PENA/)
                                                                    (WASS/)
(EDIN/)
                                                       (MEHR/)
                                          (PADI/)
                                               KEKU/
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Guo X, Shimkets RA, Padigaru M, Kekuda R, Spytek KA Topper JN, Malyankar UM, Wasserman SM, Edinger SR; Gunther E, Komuves L; Mehraban F, Topper JN, Smithson G, Gunther E,

New NOVX polypeptides and nucleic acids, useful for diagnosing or treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma, obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or multiple sclerosis.

Disclosure; SEQ ID NO 87; 215pp; English.

The invention relates to a new isolated polypeptide comprising an amino acid sequence selected from 17 fully defined human NOWX sequences (even SCO ID NGS between ADG39770 and ADG39802), a mature form of the NOWX amino acid or a variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue in the variant differs in no more than 15% of the amino acid residue in NOWX. Also included are an isolated nucleic acid (NAN) molecule comprising nucleic acid sequence encoding a NOWX polypeptide above (cod SEO ID NOS between ADG3960), a nucleic acid fragment of NOWX has a nucleic acid sequence encoding a NOWX polypeptide and a complement of NOWX has a lessence or amount of NOWX and not acid fargment of NOWX has a lessence or amount of NOWX, a method for determining che presence or amount of NOWX, a method for identifying an agent that bids to NOWX, a method for identifying an agent that be expression or activity of NOWX, a method for identifying an agent that be expression or activity of NOWX, a method for identifying an agent that be expression or activity of NOWX, a method for adentifying an agent that be expression or activity of NOWX, a method of treating or preventing a NOWX associated disorder, a method for screening for a modulator of a speciated with altered levels of NOWX or NOWX NA in a first mammal an unbject and a method of treating a pathological state in a mammal by administering NOWX or an antibody that binds to NOWX. The NOWX collappoinde, nucleic acid or antibody is useful in the manufacture of a medicament for treating a syndrome associated with a human disease or conditions associated with NOWX sequences, including cated with a meaning a nording them are useful for diagnosing or treating pathologies, diseases or conditions associated with nowX sequences, including cated with hyperplasia, prostate cancer. Industrial asthma, Coolby and sociated with a human disease, and associated of discorders, methodical asthma, coolby and sociated with

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                                                                                                                                                                   413 DIFADSLRYVNKILNSKFGFISRKVPAHMPHMIDRIVMQELQDMFPEEFDKISFHKVRHS 472
                                                                                                                                                                                                                                                                                  532
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                                                                                                                                                                                                   EDMOFAFSYFYYLMSAVOPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
                                                                                                                                         1 DIFADSLRYVNKILNSKPGFISRKVPAHMPHMIDRIVMQELQDMFPEBFDKTSFHKVRHS
                                                                                                                                                                                                                     Gaps
and in forensic identification of a biological sample. The present sequence is a protein showing sequence similarity to a NOVX protein.
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0
                                                                            Length 663;
                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                 181 NKYRFEIMGEEEIAFKMIRTNVSHVVGQLDDIRKNPRKFVC 221
                                                                           65.9%; Score 1140; DB 7; 98.6%; Pred. No. 8.3e-102; ive 1; Mismatches 2;
                                                                            Query Match
Best Local Similarity 98.6
Matches 218; Conservative
                                                  Sequence 663 AA;
                                                                                                                                                                                                                                                                121
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Search completed: November 21, 2004, 12:54:46 Job time : 39.6766 secs

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Sequence 2, Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 199613USO
CURRENT APPLICATION NUMBER: US/09/635,872A

CURRENT PILING DATE: 2000-08-10

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 1999-09-14

NUMBER: OF SEQ ID NOS: 52

SEQ ID NO 2

LENGTH: 328

HANDEL OF THE PROBLEM O
                  Sequence 155, App
Sequence 137, App
Sequence 155, App
Sequence 25, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DIFADSLRYVNKILNSKRGFISRKVPAHMPHMIDRIVMQELQDMFPEEFDKISFHKVRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTQQSGVLSDREIRTLATRIHELPLSLQDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RDFYESMFPIPSQFELPREYRNRFLHMHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFF
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US-08-469-318-137
US-08-469-318-155
US-08-469-609A-155
US-08-46-8072A-137
US-08-446-872A-137
US-08-762-227A-137
US-08-762-227A-155
PCT-US55-01185-137
PCT-US55-01185-137
US-09-538-092-596
US-09-319-232-2
US-09-351-794A-2
US-09-2248-796A-18641
US-09-2248-796A-18641
US-09-228-796A-18641
US-09-332-255-4
US-09-332-255-4
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 Query Match
Best Local S
Matches 328
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Sequence 48495, A
Sequence 10, Appl
Sequence 31, Appl
Sequence 1252, Ap
                                                                                                              November 21, 2004, 12:47:18 ; Search time 9.88676 Seconds (without alignments) 2200.144 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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US-09-636-077A-2
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US-09-636-060-2
US-09-636-077A-8
US-09-636-077A-8
US-09-636-077A-13
US-09-636-077A-13
US-09-636-077A-13
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Maximum Match 100%
Listing first 45 summaries
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; Patent No. 664203.
; General INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SEPERACE 210119030CONT
CURRENT APPLICATION NUMBER: US/09/636,060C
; CURRENT PILING DATE: 1099-09-10
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PATENT VERSION 3.1
; SASOTWARE: PATENT VERSION 3.1
; SASOTWARE: PATENT VERSION 3.1
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                     GENERAL INFORMATION:

APPLICANT: CANTELLAM

TITLE OF INVENTION: MILLIAM

TITLE OF INVENTION: MILLIAM

TITLE OF INVENTION: MILLIAM

TITLE OF INVENTION: MILLIAM

CURRENT APPLICATION NUMBER: US/09/636,077A

CURRENT FILING DATE: 2000-08-10

PRIOR PELICATION NUMBER: 60/153,831

PRIOR PLING DATE: 1999-09-19

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PALENTIN VETSION 3.0

SEQ ID NO 2

LENGTH: 328
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100.0%; Score 1731; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.5e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 1731; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.5e-168;
Matches 328; Conservative 0; Mismatches 0; Indels 0
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CRCANISM: Homo sapiens
US-09-636-060C-2
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ORGANISM: Homo sapiens
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US-09-636-060C-2
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RESULT 4

US-09-986-552-2

US-09-986-552-2

Sequence 2, Application US/09986552

Patent No. 6670165

GENERAL INFORMATION:
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, William
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

FILE REPRENEUCE: 215.08091037D1V
CURRENT APPLICATION NUMBER: US/09/986,552

CURRENT APPLICATION NUMBER: US/09/986,552

PRIOR APPLICATION NUMBER: 09/635,872

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 1999-09-14

NUMBER: OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.1

SEQ ID NO 2
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Best Local Similarity 100.0%; Pred. No. 1.5e-168;
Matches 328; Conservative 0; Mismatches 0;
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US-09-986-552-2
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EDMOFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT '120
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TITLE OF INVENTION: METHODS OF TREATING LYSOSCMAL STORAGE DISEASE
FILE REPRENCE: 1956-1050
CURRENT APPLICATION NUMBER: US/09/636,077A
CURRENT APPLICATION NUMBER: 00/00-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR RILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
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98.1%; Score 1698; DB 4;
Best Local Similarity 97.6%; Pred. No. 3.4e-165;
Matches 320; Conservative 7; Mismatches 1;
Mismatches
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320; Conservative
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ORGANISM: Mus musculus
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Best Local Similarity
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                                                                        Sequence 2, Application US/09636596C
Batent No. 6770468
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNAcase OF THE LYSOSOMAL TARGETING PATHWAY
FILE REPERENCE: 10929-0001-77
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR PILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
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US-09-635-872A-8

US-09-635-872A-8

Sequence 8 Application US/09635872A

Patent No. 6534300

GENERAL INFORMATION:
APPLICANT: CANPIELD, WILLIAM

TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
FILE REFERENCE: 195613USO

CURRENT APPLICATION WUMBER: US/09/635,872A

CURRENT FILING DATE: 2000-08-10

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.0

SEQ ID NO 8
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Pred. No. 3.4e-165;
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97.6%;
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US-09-636-596C-2
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Best Local Similarity
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US-09-635-872A-8
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TYPE: PRT
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Sequence 8, Application US/09636596C

Patent No. 6770468

GENERAL INFORMATION:
APPLICAMT: CANFIELD,
TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNAcase OF THE LYSOSOMAL TARGETING PATHWAY
FILE REFERENCE: 10929-0001-77
CURRENT APPLICATION NUMBER: US/09/636,596C
CURRENT PILING DATE: 1099-09-14
NUMBER: 0/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 8.
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Pred. No. 3.4e-165;
7; Mismatches 1;
           Score 1698; DB 4;
Pred. No. 3.4e-165;
7; Mismatches 1;
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97.6%;
                 98.1%;
             Query Match 98.1
Best Local Similarity 97.6
Matches 320; Conservative
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Best Local Similarity 97.6
Matches 320; Conservative
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US-09-636-596C-8
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APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, William
TITLE OF INFORMATION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/09/986,552
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/635,872
PRIOR APPLICATION NUMBER: 00/635,872
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEC ID NOS: 52
SOFTWARE: Patentin version 3.1
STOILD NO 8
                                                                        Sequence 8, Application US/09636060C

Patent No. 6642038

GENERAL INFORMATION:

APPLICATION:

APPLICATION GECUAC PHOSPHOTRANSFERASE OF THE LYSOSOWAL TARGETING PATHWAY

TITLE OF INVENTION: QUOMARE: US/09/636,060C

CURRENT APPLICATION NUMBER: US/09/636,060C

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PATENTIN VETSION 3.1

SOFTWARE: PATENTIN VETSION 3.1
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301 AEQIIALKRKIFPRRRIHKEASPDRIRV 328
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US-05-986-552-8
'Sequence 8, Application US/09986552
'Parent No. 6670165
                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-636-060C-8
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, ORGANISM: Mus musculus
US-09-986-552-8
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Best Local Simil
Matches 320; C
                                                      RESULT 8
US-09-636-060C-8
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Sequence 13, Application US/09986552
Patent No. 6670165
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
TILLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES
TILLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOLY APPLICATION NUMBER: US/09/986,552
CURRENT APPLICATION NUMBER: 09/635,872
PRIOR APPLICATION NUMBER: 09/635,872
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 52
SOTTWARE: Patentin version 3.1
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APPLICANT CANFELL, WILLIAM M
FULL CANFELL, CANFELL, WILLIAM M
TITLE OF INVENTION: GLCNAC PHOSPHOTRANSFERASE OF THE LYSOSOMAL TARGETING PATHWAY
TITLE OF INVENTION: GOODONT
CURRENT APPLICATION NUMBER: U5/09/636,060C
CURRENT FILING DATE: 2000-08-10
PRIOR PRILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN version 3.1
                                                                              379 YFEEVVQNCTRNLGMHLKVDTVEHSTL--VYERYEDSNLPITTRDLVVRCPLLAEALAAN 436
                                               EDMOFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT 120
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259 DIYSHSLIATNMLLNRAYGFKARHVLAHVGFLIDKDIVEAMQRRFHQQILDTAHQRFRAP 318
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ORGANISM: Drosophila melanogaster
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LENGTH: 502
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APPLICANT: CANFIELD, WILLIAM
TITE OF INVENTION:
TITE OF INVENTION: WETHOUS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSCMAL HYDROLASES FILE OF INVENTION: 195613USO
CURRENT APPLICATION NUMBER: US/09/635,872A
CURRENT FILLING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1999-09-14
NUMBER: OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
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US-09-636-077A-13
i Sequence 13, Application US/09636077A
; Betent No. 6537785;
GENERAL INFORMATION:
; APPLICANT: CANTRIELD, WILLIAM
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; TITLE OF INVENTION: METHODS OF TREATING LYSOSOMAL STORAGE DISEASE
; TITLE OF INVENTION: UNMBER: US/09/636,077A
; CURRENT APPLICATION NUMBER: US/09/636,077A
; PRIOR PILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PATENTIN VETSION 3.0
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                                               301 AEQIIALKRKIFPRRRIHKEASPDRIRV 328
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US-09-635-872A-13
; Sequence 13, Application US/09635872A
; Patent No. 6534300
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; ORGANISM: Drosophila melanogaster
US-09-635-872A-13
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LENGTH: 502
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Sequence 13, Application US/09636596C
Patent No. 6770468
GENERAL INFORMATION:
APPLICATY: CANFIELD, WILLIAM
TITLE OF INVENTION: PHOSPHODIESTER ALPHA-GLCNACase OF THE LYSOSOWAL TARGETING PATHWAY
FILE REFERENCE: 10929-0001-77
CURRENT APPLICATION NUMBER: US/09/636,596C
CURRENT FILING DATE: 2000-008-10
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE PATENTIN VETSION 3.0
SEQ ID NO 13
LENGTH: 502
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23.2%; Score 402; DB 4; Length 502;
Best Local Similarity 34.5%; Pred. No. 1.8e-32;
Matches 81; Conservative 55; Mismatches 91; Indels
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; ORGANISM: Drosophila melanogaster
US-09-636-596C-13
              ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-986-552-13
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Best Local Similarity
Matches 81; Conservi
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US-09-636-596C-13
LENGTH: 502
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November 21, 2004, 12:56:09; Search time 35.4053 Seconds (without alignments) 3280.691 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Sequence 2, Appli	Sequence 2. Appli	Sequence 5, Appli	Seguence 5, Appli	Sequence 5, Appli	'n	Sequence 5, Appli		٠.	Sequence 8, Appli			10,
		ព	US-09-895-072-2	US-09-986-552-2	US-10-023-888-5	US-10-023-889-5	US-10-023-890-5	US-10-024-197-5	US-10-023-894-5	US-10-306-686-2	US-09-895-072-8	US-09-986-552-8	US-10-023-888-10	US-10-023-889-10	US-10-023-890-10
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		Score	1731	1731	1731	1731	1731	1731	1731	1731	1698	1698	1698	1698	1698
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## ALIGNMENTS

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Sequence 2, Application US/09895072

Patent No. USZ002025550A1

GENERAL INFORMATION:
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TILL GENERAL INFORMATION:
TILL GENERAL INFORMATION:
TILL REFERENCE: 210119USOCONT
CURRENT APPLICATION NUMBER: US/09/895,072

CURRENT REPLICATION NUMBER: 60/153,831

PRIOR APPLICATION NUMBER: 60/153,831

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 1999-09-14

PRIOR FILING DATE: 2000-08-10

NUMBER: OF SEQ ID NOS: 52

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 328
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100.0%; Pred. No. 4.3e-149;
vative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 328; Conservative
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; ORGANISM: Homo sapiens
US-09-895-072-2
RESULT 1
US-09-895-072-2
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Sequence 5, Application US/10023889
Publication No. US20030124652A1
GENERAL INFORMATION:
APPLICANT: CANFIELD, William
TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARBOH
TITLE OF INVENTION: DEFICIENT CELLS
FILE REPERENCE: 203512US77
CURRENT APPLICATION NUMBER: US/10/023,889
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.1
SEQ ID NO 5.
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FILE REFERENCE: 203515US77
CURRENT PEPLICATION NUMBER: US/10/023,888
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 328
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Best Local Similarity 100.
Matches 328; Conservative
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CRGANISM: Homo sapiens
US-10-023-889-5
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CRGANISM: Homo sapiens
US-10-023-888-5
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Sequence 2, Application US/09986552
Patent No. US20020150981A1
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOWAL HYDROLASES
FILE REFERENCE: 215089US77DIV US/09986,552
CURRENT APPLICATION WUMBER: 08/09/986,552
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 09/635,872
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-09-14
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTING DATE: 1099-09-14
SEQ ID NO 2
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Publication No. US20030119088A1
GENERAL INFORMATION:
APPLICATE CANFIELD, William
TITLE OF INVENTION: SOLUBLE GLCNAC PHOSPHOTRANSFERASE
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, ORGANISM: Homo sapiens
US-09-986-552-2
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US-10-023-894-5

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Sequence 5, Application US/10023894

Publication NO. US20030143669A1

GENERAL INFORMATION:
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, Stuart
ITILE OF INVENTION: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANID)
FILE REPERBENCE: 217139US77

CURRENT APPLICATION NUMBER: US/10/023,894

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 5

LENGTH: 328

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TYPE: PRT

ORGANISM: Homo sapiens

US-10-023-894-5
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100.0%; Score 1731; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 328; Conservative 0; Mismatches 0;
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100.0%; Score 1731; DB 14;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 328; Conservative 0; Mismatches 0;
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                                              version 3.1
                                                                                                           TYPE: PRT; ORGANISM: Homo sapiens US-10-024-197-5
  CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ve
SEQ ID NO S
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Publication No. US20030124653A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION: MAMMALIAN CELLS
CURRENT APPLICATION NUMBER: US/10/023,890
CURRENT FILING DATE: 2001-12-21
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 328
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Best Local Similarity 100.0%; Pred. No. 4.3e-149; Length 328;
Matches 328; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20030133924A1
GENERAL INFORMATION:
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US-10-023-890-5
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US-10-024-197-5
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Sequence 8, Application US/09986552

Betent No. US20020150991A1

GENERAL INFORMATION:
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, William
APPLICANT: CANFIELD, William
APPLICANT: CONFIELD, WILLIAM
APPLICANT: CONFIELD, WILLIAM
APPLICANTON WUMBER: US/09/986,552
CURRENT FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
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Best Local Similarity 97.6%; Pred. No. 4.4e-146;
Matches 320; Conservative 7; Mismatches 1;
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Pred. No. 4.4e-146;
7; Mismatches 1;
CURRENT APPLICATION NUMBER: US/09/895,072
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: 60/153,831
PRIOR FILING DATE: 1998-09-14
PRIOR PLING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 52
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 8
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97.6%;
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Best Local Similarity 97.6
Matches 320; Conservative
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ORGANISM: Mus musculus
US-09-986-552-8
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; ORGANISM: Mus musculus
US-09-895-072-8
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US-09-986-552-8
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Subbication No. US20030148460A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 2303970877D1V
GURRENT APPLICATION NUMBER: US/10/306,686
GURRENT FILING DATE: 2002-31-29
PRIOR APPLICATION NUMBER: 09/636,596
PRIOR PRIOR OFFE: 0900-08-10
PRIOR PRIOR OFFE: 0900-08-10
PRIOR PRIOR OFFE: 1999-08-14
PRIOR FILING DATE: 1999-08-14
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US-09-895-072-8
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US-10-306-686-2
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SOFTWARE: Patentin version 3.1
SEQ ID NO 10
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97.6%;
                                                                                                                                                                                            Query Match
Best Local Similarity 97.6
Matches 320; Conservative
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TYPE: PRT
ORGANISM: Mus musculus
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US-10-023-890-10
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US-10-023-888-10
i Sequence 10, Application US/10023888
i Publication No. US20030119088A1
i GENERAL INFORMATION:
i APPLICANT: CANFTELD, William
i TITLE OF INVENTION: SOLUBLE GLONAC PHOSPHOTRANSFERASE
i FILE REFERENCE: 203512US77
i CURRENT APPLICATION NUMBER: US/10/023,888
i CURRENT FILING DATE: 2001-12-21
i NUMBER OF SEQ ID NOS: 38
i SOFTWARE: PatentIn version 3.1
i ENCH. 2010
i TENCH. 2010
i TENCH. 2010
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4.4e-146;
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Pred. No. 4.4e-
7; Mismatches
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Publication No. US20030124652A1
GENERAL INFORMATION:
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ilarity 97.6%;
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US-10-023-888-10
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US-10-023-889-10
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APPLICANT: CANFIELD, William

'TITLE OF INVENTION: METHODS OF PRODUCING HIGH MANNOSE GLYCOPROTEINS IN COMPLEX CARBC

TITLE OF INVENTION: DEFICIENT CELLS

TITLE OF INVENTION: DEFICIENT CELLS

CURRENT APPLICATION WHOBER: US/10/023,889

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 21

SOFFWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 328

TYPE: FRT

TYPE: FRT

CREANISM: Mus musculus

CREANISM: Mus musculus

CREANISM: Mus musculus
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Publication No. US20030124653A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD OF PRODUCING GLYCOPROTEINS HAVING REDUCED COMPLEX CARBOH)
TITLE OF INVENTION: MAMMALIAN CELLS
FILE REPRENCE: 203510US77
CURRENT APPLICATION UNDER: US/10/023,890
CURRENT APPLICATION UNDER: 2001-12-21
NUMBER OF SEQ ID NOS: 21
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Pred. No. 4.4e-146;
7; Mismatches 1;
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Search completed: November 21, 2004, 13:22:35 Job time : 36.4053 secs
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US-10-024-197-10

US-10-024-197-10

Sequence 10, Application US/10024197

Publication No. US20030133924A1

GENERAL INFORMATION:

APPLICANT: CANFIELD, William

TITLE OF INVENTION: HIGHLY PHOSPHORYLATED ACID BETA-GLUCOCEREBROSIDASE AND METHODS (FILLE REFERENCE: 209794USO)

CURRENT APPLICANTION: US/10/024,197

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NO 100

SEQ ID NO 100
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                                                          NKYRFEIMGEEEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVL 240
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US-10-023-894-10
Sequence 10, Application US/10023894
Publication No. US20030143669A1
GENERAL INFORMATION:
APPLICANT: CANFIELD,
APPLICANT: KORNFELD, Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus
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TITLE OF INVENTION: EXPRESSION OF LYSOSOWAL HYDROLASE IN CELLS EXPRESSING PRO-N-TITLE OF INVENTION: ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYL GLUCOSIMANIDAS FILE REFERRENCE: 217139US77
CURRENT APPLICATION NUMBER: US/10/023,894
CURRENT FILING DATE: 201-12-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENLIN VEXSION 3.1
SSOFTWARE: PATENLIN VEXSION 3.1
SEQ ID NO 10
LENGTH: 328
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Pred. No. 4.4e-146;
7; Mismatches 1;
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Best Local Similarity 97.6%;
Matches 320; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Mus musculus
US-10-023-894-10
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November 21, 2004, 12:39:03 ; Search time 10.0204 Seconds (without alignments) 3149.495 Million cell updates/sec
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1731
1 DTFADSLRYVNKILNSKFGF......RKIPPRRRIHKEASPNRIRV 328
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000 PIR 79:\*
1: Dir1:\*
2: Dir2:\*
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4: Dir4:\* 1 2 8 4 Database :

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AI2886	F97662	A25281	B71619	D83706	B71614	S63033	S37049	D96594	DJVZ4I	T30802	T15564	D69681	AH1888	RGNVE2	E72868
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93	66	92.5	92.5	92	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	16	91	91
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

T50618 hypothe Cjpothe CjDate: C,Acces R,Bloce R,Bloce R,AAcces A,Acces A,Acce	### ### ##############################
Maes	os; score 1290; DB 2; Dengun 248 .0%; Pred. No. 7.6e-87; 0; Mismatches 0; Indels
ζ 00 02	85 VFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLTGLEHMLINCSKMLPADITQLNNIP 144
දු දු	145 PIQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDKOKYRREIMGEEIAFKOIRTNVSH 204
Q7 Dp	205 VVGGLDDIRKNPRKEVCLNDNIDHNHKDAQTVKAVLRDFYBSMFPIPSQFELPREYRNF 264
දු දු	265 LHWHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFFAEQLIALKRKIFPRRIHKEASPN 324
යි යි	325 RIRV 328       245 RIRV 248
RESULT 149528 hypoth N,Alte C,Spec C,Date C,Acce R,Cord	RESULT 2 Hy952B Hy953B Hy95B Hy953B H

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6.4%;
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Best Local Similarity
Matches 47; Conservi
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NyAlernate names: procein N0872; protein YNL250w
C;Species: Saccharomyces cerevisiae
C;Date: 31-Dec-1991 #sequence_revisiae
C;Alani, E.; Subbiah, S.; Kleckner, N.
Genetics 122, 47-57, 1899
A;Title: The yeast RAD50 gene encodes a predicted 153-kD protein containing a purine nuc
A;Reference number: S05808; MUID:89276917; PMID:2659437
A;Accession: S05808; MUID:89276917; PMID:2659437
A;Accession: S05808
A;Molecule type: DNA
A;Residues: 1-1312 calabor, U; Beinhauer, U; Fiedler, T; Hegemann, U;H.
R;Sen-Gupta, M; Gueldener, U;Beinhauer, U;Fiedler, T; Hegemann, U;H.
R;Sen-Gupta, M; Gueldener, S63220
A;Accession: S6323
A;Acc
A,Title: The mouse segmentation gene kr encodes a novel basic domain-leucine zipper tran A,Reference number: A55200; MUID:95094266; PMID:8001130
A,Accession: I49528
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-384 <RES>
A;Cross-references: UNIPROT:Q61340; GB:L36434; NID:g625041; PIDN:AAA65688.1; PID:g625042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.2%; Score 124; DB 1; Length 1312;
21.3%; Pred. No. 0.54;
trive 65; Mismatches 126; Indels 60;
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0
                                                                                                                                                                                                                            Length 384;
                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                       33.6%; Score 581; DB 2;
.larity 97.4%; Pred. No. 5.9e-35;
Conservative 2; Mismatches 1;
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Best Local Similarity 21.3
Matches 68; Conservative
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Best Local Similarity
Matches 112; Conserv
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Upobable capsule biosynthesis protein NWA0200 [imported] - Neisseria meningitidis (straignobable capsule biosynthesis protein NWA0200 [imported] - Neisseria meningitidis C;Species: Naisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 [Accession: C82014 | A. Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000 | A.Reference number: A81775; MUD:20222556; PMID:10761919 | Neisseria menigitidis Z2491. A.Residues: Complete DNA A.Residues: 1-545 < PAR> A.Residues: 1-54
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C.Species: Plasmodium falciparum (C.Species: Plasmodium falciparum (C.Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 (C.Accession: T18414 A.H.; Symons, F.; Van Driel, R.; Cappai, R. Mol. Blochem. Parasitol. 74, 143-156, 1995 A.F. Handman, E.; Osborn, Parasitol. 74, 143-156, 1995 A.F. Handman A.F. Leishmania promastigote surface antigen 2 complex is differentially. Reference number: 218933; MulD:96360472; PMID:8719156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
226 IDHNHKDAQTVKAVLRDFYESMFPIPSQFELPREYRNRFLH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.6%; Score 113.5;
18.4%; Pred. No. 1;
cive 36; Mismatches
                                                                                                                                                                                                                                                               |||: : |::||: |
469 SLNHELENLKTYKEKLQSW 487
                                                                                                                                                                                                267 -- MHELQEWRAYRDKLKFW 283
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A; Molecule type: mRNA
A; Residues: 1914-1998, I' <8U2>
A; Experimental source: brain
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Reywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleot
F; 84-75/Domain: myosin motor domain homology 
F; 84-75/F Region: actin binding #status predicted
F; 83-1999/Domain: cotin binding #status predicted
F; 83-1276/Region: 120
F; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PHO176 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Satesion: F1239
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekra, O, Ohitu, Y.; Funahashi, T.; Tanaka, T.; Kidoh, Y.; Yamazaki, J.; Kushida, N.; Oguci DNA, Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-690 «KM»
A;Cross-references: UNIPPOT:057915; GB:AP000001; NID:g3236128; PIDN:BAA29245.1; PID:g3;
A;Cross-references: uniphaces an interim accession for a sequence replaced by GenBan)
                                                                                                                                                                         heavy chain from mammalian bra
                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebra
                                                                                                                                                                                                                                A;Accession: S21801
A;Molecule type: mRNA
A;Residues: 1-1999 «SUNA
A;Cross-references: UNIPROT:Q63731; EMBL:X62659
R;Sun, W.; Chantler, P.D.
Biochem. Biophys. Res. Commun. 175, 244-249, 1991
A;Title: A unique cellular myosin II exhibiting differential expression in the A;Reference number: PN0013; MUID:91151356; PMID:1998509
A;Accession: PN0013
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   C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession. S21801; PN0013; S18134
R;Sun, W.; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 VIKSLVTNCKPVTDKIHKAYKDKNKYRPEIMGEEEIAFKMIRTNVSHVVGQLDDIRKNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 KFV-CLNDNIDHNHKDAQTVKAVLRDFYESM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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6.0%; Score 104.5;
Best Local Similarity 26.5%; Pred. No. 24;
Matches 40; Conservative 29; Mismatches
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GTP-binding protein - cherry salmon
GTP-binding protein - cherry salmon
C;Species: Oncorbymchus masou (cherry salmon)
C;Gpecies: Oncorbymchus masou (cherry salmon)
C;Accession: T00394
C;Accession: T00394
C;Accession: T00394
C;Accession: T00394
A;Atitle: Isolation of a cDNA for a novel 120-kDa GTP-binding protein expressed in motor
A;Atitle: Isolation of a cDNA for a novel 120-kDa GTP-binding protein expressed in motor
A;Accession: T00394
A;Accession: T00394
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-971 < KUB>
A;Cross-references: UNIPROT:093248; EMBL:AB012720; NID:g3413519; PIDN:BAA32279.1; PID:g3
A;Cross-references: UNIPROT:093248; EMBL:AB012720; NID:g3413519; PIDN:BAA32279.1; PID:g3
C;Keywords: GTP binding; nucleotide binding motif A (P-loop)
F;307-314/Region: mucleotide-binding motif A (P-loop)
      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GLEHMLINCSKWIPPDITQINNIPPTQESYYDPNIPPVTKSLVTNCKPVTDKIHKAYKDK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 NKYRFEIMGEEEIAFKMIRTNVSH--VVGQLDDIRKNPRKFVCLNDNID-HNHKDAQTVK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 --REIR----TLATRIHELPLSLQ-----DLTGLEHMLINCSKMLPADITQLNNIPP--
                                                                                                                                                                                                                                                        1309 KFQEIROHMRDKIENTIHELYKEMYVQIQIDLINYYHQLENIHSELLQALQQNKNIPRHL
                                                                                                                                                                                                                                                                                                                          -----TQESYYDPNLPPV-TKSLVTNCKPVTDKIHKAYKD-----KNKYRFEI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHKDAQ-----TVKAVLRDFYESMFPIPSQFELPREYRNRFLHMHELQEWRAYRDKLK
                                                              41 LODMFPEEFDKTSFHKVRHSEDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSD-
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      88;
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      94; Indels
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AVLRDFYESMFPIPSQFE-----LPR 258
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50;
Conservative
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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A Experimental Source: strain 5288C

Ribu, Z.

Submitted to the EMBL Data Library, July 1995

A, Description: The sequence of S. cerevisiae cosmid 9798.

A, Reference number: 859418

A, Reference number: 859418

A, Residues: 15518

A, Residues: 15518

A, Crosser-references: EMBL:U32517; NID:9914989; PIDN:AAB64759.1; PID:9915000; MIPS:YDR3236

A, Residues: 15518

A, Residues: 15518

A, Residues: 15518

A, Reference number: A1756; MUID:92112720; PMID:1730622

A, Residues: 1-365, YY, 367-515 (WEL)

A, Residues: 1-365, YY, 367-515 (WEL)

A, Residues: 1-365, YY, 367-515 (WEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:U22070; NID:9736413; PIDN:AAB60290.1; PID:9736
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A.Cross-references: SCD:S0002731; MIPS:YDR323c
A.Map posttion: 4R
C.Function: A.Penction: A.Penction and vacuolar protein sorting; required
                                                                                                                                                                          vacuolar segregation protein PEP7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D9798.11; protein YDR323c; vacuole segregation protein VAC1
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13.43n-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S59811; S59789; A41756
R;Webb, G.C.
submitted to the EMBL Data Library, March 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: M80596; NID: g173156; PIDN: AAA35203.1; PID: g173157
       263 RFLHM-HELQEWRAYRDKLKFWTHCVLATLIMFTIFSFFAEQLIALKRKIF 312
                                          414 NPINIKSELDKNNSEKFKL-----TLBIDFNFGIFBFFFB----LFRSIF 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Sumerfamily: vacuolar segregation protein PBP7 C; Keywords: DNA binding; yeast vacuole; zinc finger F;8-29/Region: zinc finger CCHH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 102; DB
ilarity 22.8%; Pred. No. 6.6;
Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                        A,Reference number: S59811
A,Accession: S59811
A,Molecule : 1798: DA
A,Reduces: 1-515 <WEB>
A,Cross-references: UNIPROT: Q99229;
A,Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 NHKDAQTVKAVLRD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||::||
498 LHSRIHTVQSKLGD 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281 HIPISIRLCSHCIDML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 58; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 L----
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                  8 8
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D90124
C, Species and Comported 1 - Guillardia theta nucleomorph
C, Species and Computed 2 - Guillardia theta nucleomorph
C, Species and Computed 3 - Guillardia theta the vestigial nucleus of a cukaryotic endosymbiont
A; Note: a nucleomorph is the vestigial nucleus of a cukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Uul-2004
C; Accession: D90124
R; Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
R; Douglas, S.; Zauner
R; Douglas, S.; Zauner
R; Douglas, S.; Zauner
R; Douglas, S.; Zauner
R; Nature 410, 1091-1096, 2001
A; Title: The highly reduced genome of an enslaved algal nucleus.
A; Reference number: A99082; MUID:1132671; PMID:1132671
A; Accession: D90124
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-706 < DOU>
A; Cross-references: UNIPROT:Q98S94; GB:AF083031; NID:g13794312; PIDN:AAK39689.1; GSPDB:G
C; Genetics:
A; Gene: rad3
A; Gene: rad3
A; Gene: rad3
A; Gene: rad3
A; Geneme: nucleomorph
C; Keywords: nucleomorph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIEIAPVYFQNFNDNISHYCKTYSFFDNKSLNGIKKI-----SNFLILTKFFL--NYQN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLDVIRSSINSKFDFVNKFKLKPNCNFYINFLLKKRKIYKNYIDTRKILKFSRNNKVCPY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RILATRIHELPLSLQDLTGLEHMLINCSKMLPADITQLNNIPPTQESYY-DPNLPPVTK 160
                                                                                                                 ----IPFEKVKRRYESK 399
                                                                                                                                                                     124
                                                                                                                                                                                                  DKI-----HKAYKDKNKYRFEIMGEE---EIAFKMIRTNVSHVVGQLDDIRKNPRKFV 220
                                                                                                                                                                                                                                                                                                                                                                                                  221 CLNDNIDHNHKDAQTVKAVLRDFYESMFPIPSQFELPREYRN----RFLHMHELQEWRAY 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 LKTIIDSYRSLIIVERDIIKKKIFQINVLK-----TFNNFHLKKNFFYIKKNKKILNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLVINCKPVTDKIHKAYKDKNKYRFEIMGEEBIAFKMIRINVSHVVGQL-----D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FHKVRHSEDMQFAFSYFYYLMSAVQPLNISQ-----VFDEVDTDQSGVLSDREI----
                                                                                                                                                                     65 FAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLTGLEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 SLRYVNKILNSKFGFISR-KVPAHMPHMID-----RIVMQELQDMFPEBFDKTS----
                                                                 5 DSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHSEDMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
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                       Indels
                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144;
                     114;
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  Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 RD-----KLKFWTHCV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDTFMSLPAIPLKFWNNVV 620
                          55;
  20.7%;
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                          Conservative
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Best Local Similarity
Matches 66; Conserv
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immediate early protein - Bombyx mori nuclear polyhedrosis virus
() Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
() Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
() Accession: $20596
() Accession: $20596
() Accession: $20596
() Aritle: Nucleotide sequence of a transactivating Bombyx mori nuclear polyhedrosis virual Areference number: $20596
() MJD:92162753; PMID:1536885
() Accession: $20596
() MJD:92162753; PMID:1536885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 PNLPPVTKSLVTNCKPVTDKIHKAYKDKNKY----RFEIMGEEEIAFKMIRTNVSHVVG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ELPLSLQDLTGLEHMLINCSK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 MLPADITQLNNIPPTQBSYYDPNLPPVTKSLVT-----NCKPVTDKIHKAYKDKNKY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : ||: : ||| : 307 CHFVDVH--HTFKAALISYENLDMYYAQTIFVTLLQSLGERKCGFLLSKLYEMYQDKNLF 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 RFEIM-----GEEEIAFK--MIRTNVSHVVGQLDDIRK-----NPRKFVCLNDNIDHN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 TLPIMLSRKESNEIETASNNFFVSPYVSQILKYSESIRKVKFPDNPPNKYVVDNLNLIVN 424
                                                                                                                                                                                                                                                 2028 ----SLEEIRIVÄKERDELRRIKESLKMERDOFIATLREMIÄRDRQNHOVKPEKRLLSD
                                                                                                                                                                                                      33 IDRIVMQELQDMFPEEFDKTSFHKVRHSEDMQFAFSYFYYLMSAVQPLNISQVFDEVDTD
                                                                                                                                                                                                                                                                                                                                            QSGVLSDREIRTLATRIHELPLSLQDLTGLEHMLINCSKMLPADITQLNNIPPTQESYYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2083 -GQQHLMESLREKCSRIKELL-KRYSEMDDHYECLNRLSLDLEKBIEFHRIMKKLKYVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 VVYEY-TNNYYMVDNRVFVVTFDKIRFMISYNLVKETGIBIPHS-QDVCNDETAAQNCKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1199 LHIEBILKDFSESBFPSIKTEFQ--QVLSNRKEMTQFLEEWLNTRFDIEKLK 2248
                                                                                                                                         58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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                                                                    Length 2663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 QLDDIRKNPRKFVCLND-------NIDHNHKDAQT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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; Pred. No. 12;
34; Mismatches 103;
                                                                                                                                     127;
                                                                    DB 1;
                                                                                                                                     47; Mismatches
                                                                                                     62;
F;92/Binding site: ATP (Lys) #status predicted
                                                                5.8%; Score 101; 20.5%; Pred. No. 6
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A61231
myosin heavy chain nonmuscle form A - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%;
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                                                                                                                                     Conservative
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                                                                                          Best Local Similarity
Matches 60; Conserv
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                                                                    Query Match
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                                                                               probable membrane protein Im00559 [imported] - Listeria monocytogenes (strain EGD-e) c'Species: Listeria monocytogenes C'Species: Listeria Miller C'Accession: AH1144 R'Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. D.; Nunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Macok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUD:21537279; PMID:11679669
A; Accession: AH1144
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-301 cGLA>
A; Cross-references: UNIPROT: QBYGS9; GB:NC_003210; PIDN: CAC98638.1; PID:g16409935; GSPDB: A; GGmetics: Lmo0559
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A;Residues: 1-2663 <YEN>
A;Cross-references: UNIPROT:Q02224; EMBL:Z15005; NID:g29864; PIDN:CAA78727.1; PID:g29865
C;Genetics:
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A; Map position: 4q24-4q25
C; Superfamily: centromere protein E, kinesin motor domain homology
C; Superfamily: centromere protein E, kinesin motor domain; nicrotubule binding; mitosis; nucleotide binding; P-loop
F; 7-335/Domain: kinesin motor domain homology < KMOT>
F; 86-93/Region: nucleotide-binding motif A (P-loop)
F; 486-2183/Domain: coiled coil #status predicted <COI>
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NyAlternate names: centromere 312K protein, kinesin-related protein CENP-B
C;Species: Homo sapiens (man)
C;Decies: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C;Accession: S28-539, 1992
A;Yen, T.J.; Li, G.; Schaar, B.T.; Szilak, I.; Cleveland, D.W.
Nature 359, 535-539, 1992
A;Title: CENP-E is a putative kinetochore motor that accumulates just before mitosis.
A;Reference number: S28261; MUID:93024922; PMID:1406971
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20.2%; Pred. No. 3.7;
ive 44; Mismatches
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| IVTIFISVILWFGLSFILRKLM 300
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Best Local Similarity 20.2%
Matches 53; Conservative
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-715 sSINA
A;Kesidues: 1-715 sSINA
A;Cross.references: UNIPROT:P35579; UNIPROT:Q9UMJO; GB:M69180; NID:g189029; PIDN:AAA6176
B;Saez, C.G.; Myers, J.C.; Shows, T.B.; Leinwand, L.A.
Proc. Natl. Acad. Sci. U.S.A. 87, 1164-1168, 1990
A;Title: Human nonmuscle myosin heavy chain mRNA: generation of diversity through altern A;Reference number: A34876; MUID:90138958; PMID:1967836
N;Alternate names: cellular myosin heavy chain; myosin type 9; NMMHC-A
N;Contains: myosin ATPase (BC 3.6.4.1)
C;Species: Homo sapiens (man)
C;Date: 12-May-1994 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A61231; A34876; Ī52562; I61692
C;Accession: M.; Wang, M.; McBride, O.W.; Kawamoto, S.; Yamakawa, K.; Gdula, D.; Adelstein, Circ. Res. 69, 530-539; 1991
A;Title: Human nonmuscle myosin heavy chains are encoded by two genes located on differe A;Reference number: A61231; MUID:91316803; PMID:1860190
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A; Residues: 715-1961 < SAE>
A; Residues: 715-1961 < SAE>
A; Cross-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036
A; Cross-references: GB:M31013; NID:g189035; PIDN:AAA36349.1; PID:g189036
B; Tochaker, L.E.; Gonzalez, D.A.; Tung, N.; Lemons, R.S.; Le Beau, M.M.; Arnaout, M.A.;
Blood 78, 1826-1833, 1991
A; Title: Callular myosin heavy chain in human leukocytes: isolation of 5' cDNA clones, CA; Reference number: I52562; MUID:92003925; PMID:1912569
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Rolecule type: mRNA
A,Residues: 1-52, 'BAI', 56-659, 'T', 661-868, 'T', 870-930,'C', 932-1239,'KG',1242-1337 <RB'
A,FCross-references: GB:N81105; NID:g1888988; PIDN AAAS9888 1; PID:g553596
A,FBement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994
A,FILLE: Identification and overlapping expression of multiple unconventional myosin (A,Reference number: A55758; MUID:94294418; PMID:8022818
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A;Molecule type: mRNA
A;Residues: 152-218 «BEM»
A;Residues: 162-218 «BEM»
A;Cross-references: GB:L29141; NID:g457249; PIDN:AAA20904.1; PID:g531134
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metryl-accepting chemotaxis protein (mcp-3) homolog - Lyme disease spirochete C.Species: Borrelia burgdorferi (Lyme disease spirochete)
C.Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C.Date: Daylon, B. Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, S. Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. A.Authors: Smith, H.O.; Venter, J.C.
A.Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A.Reference number: A70100; MUID:98065943; PMID:9403685
A.Accession: D70174
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A;Nolecule Type: DNA
A.Residues: 1-735 - KLE>
A.Cross-references: UNIPROT:O51543; GB:AE001161; GB:AE000783; NID:g2688515; PIDN:AAC6695
A.Experimental source: strain B31
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 18.4 les 47; Conservative
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Minimum DB seq Maximum DB seq

Database

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Aat03370 listeria
Q63731 rattus norv
Q8138 plasmodium
Q8K839 streptococc
Q7rrc2 plasmodium
Q81310 bacillus ce
O57915 pyrococcus
Q6557915 pyrococcus
Q7xx3 cryptospori
Q98594 quillardia
Q6877 plasmodium
Aao38041 plasmodium
Aao38041 plasmodium
Q99229 saccharomyc.
Q8y999 listeria mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 DIFADSLRYVNKILNSKFGFISRKVPAHMPHMIDRIVNQELQDMFPEEFDKISFHKVRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLEHMLINCSKWLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLEHMLINCSKMLPADITQLNNIPPTQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 NKYRFEIMGEEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DTFADSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                    Q86TQ2 PRELIMINARY, PRT; 490 AA.
01-JUN-2003 (TERMELrel: 24, Created)
01-JUN-2003 (TERMELrel: 24, Last sequence update)
01-JUN-2004 (TERMELrel: 26, Last annotation update)
Similar to v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (Avian) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Liver;
Strausberg R.;
Strausberg R.;
Submitted (GAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BC042615; AA442615.1; ---
R GO; GO:0005509; F:calcium ion binding; IEA.
R InterPro; IPR010506; DMAP binding.
R InterPro; IPR010593; EF-hand.
R InterPro; IPR010593; EF-hand like.
Pfam; PF06464; DMAP_binding; 1.
R Pfam; PF06464; DMAP_binding; 1.
R Pfam; PF06515; efhand; 1.
R Pfam; PF003018; EF_HAND; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1731; DB 2; Length 100.0%; Pred. No. 2e-120; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57411 MW; 37B19FE0D1259AD2 CRC64;
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                   Q63731

Q81188

Q81188

Q7RRZ2

Q7RRZ2

Q6813R0

Q57915

Q6 BFN4

Q6 BFN4

Q9 8 S94

AAQ38041
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Matches 328; Conservative
  301
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      Homo sapiens
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SEQUENCE
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Q9nyy homo sapien
Q74096 anopheles g
Q9v553 drosophila
Q9sxi4 drosophila
Q9sxi4 drosophila
Q6sxi4 drosophila
Q6sxi4 drosophila
Q6jut9 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Aaq74772 pichia angla
Q6szi5 neisseria m
Q83u50 neisseria m
Q8100 neisseria m
Q8100 neisseria m
Q8100 neisseria m
Q1000 neisseria m
Q26c23 plasmodium
Q26c23 plasmodium
Q1000 dictyosteli
Q93u8 oncorhynchu
Q86km0 dictyosteli
Q93u8 oncorhynchu
Q86km0 dictyosteli
Q93u8 physarum po
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homo sapien
mus musculu
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Aah60638 mus muscu
                                                                                                                             November 21, 2004, 12:46:58; Search time 47.0289 Seconds (without alignments) 4012.911 Million cell updates/sec
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                                                                                                                                                                                                                                                     1 DTFADSLRYVNKILNSKFGF.......RKIFPRRRIHKEASPNRIRV 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q86tg2
Q9ull2
              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                         1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Q61340
Q90098
Q9V553
Q8SXI4
RA50 YEAST
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OPA1 ONCMA
EZRA STRPY
Q9MJ79
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Maximum Match 100%
Listing first 45 summaries
                                                                                           - protein search, using sw model
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Q9ULL2
Q6P9R5
AAH60638
Q9NPW9
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AAQ74772
Q63155
Q683159
Q84020
Q84000
Q940W8
Q26033
Q26857
Q61473
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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1731
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Match Length
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Score

342

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AEQLIALKRKIFPRRRIHKEASPNRIRV 328

RDFYESMFPIPSQFELPREYRNRFLHMHELQEWRAYRDKLKFWTHCVLATLIMFTIFSFF

241 403 301

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physarum po physarum po xenopus lae listeria mo

Q9BJD3 Q90XS4 Q722Z1

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schwafer C.P., Bhat N.K.,

Altschul S.F., Zeeberg B. B. Bonaldo M.S. II, Wang J., Haiteh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casrainci P., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley V.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Jones S.J., Marza M.A.,

M. Jones M. J., More C., Manalysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 DIFADSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQELQDMFPEEFDKTSFHKVRHS 653
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                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.1%; Score 1698; DB 2; Length 9:
97.6%; Pred. No. 1.3e-117;
ive 7; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stransberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; BEC66638, AAH60638,1;
InterPro; IPR002048; EF hand.
InterPro; IPR008083; EF Hand_like.
InterPro; IPR008060; Notch_region.
Pfam; PF00066; efhand; 1.
Pfam; PF00066; Notch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     921 AA; 104970 MW; 12879CDE978D87BB CRC64;
                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00004; NL; 2.
PROSITE; PS00018; BF_HAND; UNKNOWN_1.
                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
             05-UUL-2004 (TERMBLRE1. 2
05-UUL-2004 (TERMBLRE1. 2
05-UUL-2004 (TERMBLRE1. 2
Hypothetical protein.
Mus musculus (Mouse).
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                                                                                                                                                                                        NCBI_TaxID=10090;
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MEDILINE=20039619; PubMed=10574462;

Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.;

The accomplete sequences of unidentified human genes. XV.

The complete sequences of 100 new cDNA clones from brain which code

for large proteins in vitro.";

IDNA Res. 6:337-345(1999).

IE BMBL; AB033034; BA486522.2;

RGO; GO:0016020; C:membrane; IEA.

RGO; GO:0016209; F:calcium ion binding; IEA.

RGO; GO:0030154; P:cell differentiation; IEA.

RINE-PRO; IPR010506; DMAP Dinding.

RINE-PRO; IPR008000; Notch region.

Pfam; PF00464; DMAP_Dinding; 1.

Pfam; PF00466; PMAP_Dinding; 1.

Pfam; PF00466; PMAP_Dinding; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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100.0%; Pred. No. 4.7e-120;
iive 0; Mismatches 0;
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463 AEQLIALKRKIFPRRRIHKEASPNRIRV 490
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                                                                                                                                                                        Q9ULL2;
01-MAY-2000 (TrEMBLrel. 13, C;
01-OCT-2002 (TrEMBLrel. 22, L;
01-MAR-2004 (TrEMBLrel. 26, L;
KIAA1208 protein (Fragment).
Name=KIAA1208;
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145 PIQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDKNKYRFBIMGBEBIAFKMIRTNVSH 204
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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INTERPOSE TSOG18.
INTERPOSE IPRO20248, EF-hand.
Interpro; IPRO10983; EF-hand.
PROSITE, PSOG18, EF-HAND, UNKNOWN.1.
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                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp762B226 (Fragment).
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
1-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ10959.
Homo sapiens (Human).
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100.0%; Pred. No. 5.6e-88;
ive 0; Mismatches 0;
                                                                                                                                                                                                                           248 AA
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 244; Conservative
                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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SEQUENCE FROM N.A.
TISSUE=Placenta;
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SEQUENCE FROM N.A.

STRAIN=C578H/6/ ITSSUE=Erain;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachard S.P., Zeeberg B. Duetow K.H., Schaefer C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Duetow K.H., Schaefer C.F., Bhat N.K.,

RA HOpkins R.F., Jordan H., Moore T., Marg J., Hashe F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Worlan T.B., Tochiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Holton B., Ketteman M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Wiltalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Halton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RAZYWINSKI M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

T. "Generation and initial analysis of more than 15,000 full-length human

RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKYRFEIMGEBEIAFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNIDHNHKDAQTVKAVL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDFYESMFPIPSQFELPREYRNRFLHMHELQEWRAYRDXLKFWTHCVLATLIMFTIFSFF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDMQFAFSYFYYLMSAVQPLNISQVFDEVDTDQSGVLSDREIRTLATRIHELPLSLQDLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDFYESMFPIPSOFELPREYRNRFLHMHELOSWRAYRDKLKFWTHCVLATLIIFTIFSFF 893
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                                                                                                                                                                                                                                               02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AAH60638.1; -- Hypothetical protein. SEQUENCE 921 AA; 104970 MW; 12879CDE978DB7BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.1%; Score 1698; DB 2;
97.6%; Pred. No. 1.3e-117;
iive 7; Mismatches 1;
                                                                                                                                                                                        921 AA
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 97.6
Matches 320; Conservative
                                                                                                                                                                                     PRELIMINARY;
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02-MAR-2004
02-MAR-2004
                       894
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Length 384;

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267 DIFADSLRYVNKILNSKFGFISRKVPAHMPHMIDRIVNQELQDMPPEEFDKISFHKVRHS 326
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PIR; 149528; 149528.

WGD; MGI:104555; Mafb.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0005677; C:transcription factor complex; IDA.
GO; GO:0005677; F:DNA binding; IDA.
GO; GO:0005777; F:DNA binding; IPI.
GO; GO:0005777; F:Protein binding; IPI.
GO; GO:0007585; P:respiratory gaseous exchange; IMP.
GO; GO:0007379; P:segment specification; IMP.
InterPro; IPR010506; DNAP binding.
InterPro; IPR010506; DNAP binding.
InterPro; IPR010506; Pland.
InterPro; IPR010506; Pland.
InterPro; IPR010506; Pland.
InterPro; IPR010506; Pland.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 EDMOFAFSYFYYLMSAVQPLNISQVFHEVDTDQSGVLSDREIRTLATRIHDLFLT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 33.6%; Score 581; DB 2; Length 38. Local Similarity 97.4%; Pred. No. 5.3e-35; es 112; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 553; DB 2; Length 71 39.6%; Pred. No. 1.46-32; Live 57; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         384 AA; 43753 MW; 51F473C8807A7E55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 AA; 82794 MW; 0BA7D2B957E48250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgCP9986 (Fragment).
Name=agCG49111; ORFNames=ENSANGG0000017588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          717 AA.
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NON TER 1
SEQÜENCE 384 AA; 43753 MW: 517477
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EMBL, AAAB01008986; EAA00384.1; -.

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NON TER 717 717

SEQUENCE 717 AA; 82794 MW; 0BA
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                    RA YOURGESTAND YOUR STATE OF SURE TO, SUBJYAME TO, ITIE R., RAKEMERS A., Hayashi K., Satch. Nagai K., Kimura K., Makira H., Sachine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Sehine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Ramanoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Raduch H., Hosoiri T., Kavai Y., Kodaira H., Sugawara M., Atakahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Rahibashi T., Yamashita H., Murakawa K., Fujimori K., Anata H., Kinata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S., Anehori K., Takiguchi S., Matanabe M., Hiraoka S., Chiba Y., Ishida S., Ranehori K., Takiguchi S., Matanabe S., Yosida M., Hotuta T., Kusano J., R. Araehori K., Takiguchi S., Matanabe S., Yosida M., Arita M., Momos N., R. Araehori K., Yuti H., Oshima A., Sasaki N., Aotsuka S., Moniyama H., Satoh N., Takami S., Terashima Y., Sano S., Noshikawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Rhibagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Rhibagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Sugiyama A., Takemoto M., Kawakami B., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Sudasa A., Hikiji T., Kobateke N., Inagaki H., Ikanabe K., Kukakami T., Kopama M., Tashiro H., Nomura Y., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Matahi W., Wamana M., Kikuchi H., Mataho Y., Yamashita R., Nakai K., Yada T., Nomura N., Kikuchi H., Mataho Y., Sasaki M., Matahi W., Wamana W., Matamura Y., Ohara O., Isoati T., Sugano S., Nakai K., Yada T., Nagase T., Nomura N., Kikuchi H., Masuho S., R., Rowalami Y., Ohara O., Isoaga T., Sugano S., Ohana W., Masamura Y., Ohara O., Isoaga T., Sugano S., Chana W., Masamura Y., Ohara O., Isoaga T., Nowasa M., Saraki M., Saraki M., Saraki M., Saraki M., Saraki
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Basic domain/leucine zipper transcription factor (Fragment).
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EMBL; AK001821; BAA91926.1; -.
SEQUENCE 132 AA; 16083 MW; 92B5DEB4E062AD07 CRC64;
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Pred. No. 9.9e-45;
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Matches 132; Conservative
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           PubMed=14702039;
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REDURINES COLORIOR PROMPHER S.L. LIF W., HOSKINS R.A., Galle R.F.,

REDURING R.C., ROGERS Y. H., Richards S., Ashburner M., Henderson S.N.,

RENDING R.C., ROGERS Y. H., Black B.C., Champe M., Pfeiffer B.D.

RAM K.H., LOYJE C., BAXER E.G., Hell G., Nelson C.R., Galbor G.L.,

Abril U.F., Adbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RAM K.H., LOYJE C., BAXER E.G., Hell G., Nelson C.R., Galbor G.L.,

Abril U.F., Doyle C., Baxer E.G., Hell G., Nelson C.R., Galbor G.L.,

Abril U.F., Doyle C., Baxer E.G., Hell G., Nelson C.R., Galbor D.,

RAM E.G., C., Busam D.A., Bunck J., Brockstein P., Borther P.,

Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dohnke C., Davenport L.B., Davies P.,

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Cherry J.M., Laviery D., Heimen T.J., Herrandes J.R., Houck J.,

RAM E.G., Mong P., Gorrell J.H., Gu Z., Galbart W.M., Glasser K.,

RAM E.G., Lei Y., Leviteky A.A., Li J., M. J., Li J., Li J.,

RAM E.G., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

Anaktei B. M. Mollon K., Murphy B., Murphy D.M., Moshrefi A.,

RAM E.G., Lei Y., Remington K., Saunders R.D., Pollard J., Pull Y., Rector C.,

RAM E.G., Stden-Kiamos I., Simpson M., Strong R., Sun B.,

Shie B.C., Sheden-Kiamos I., Simpson M., Strong R., San H.,

She B.C., Shen H.M., Pittman G.S., Pan S., Pollard J., Wang S., Sun B.,

Shie B.C., Shend-Kiamos I., Shapon M., Strong R., Sun B.,

Shie B.C., Shend-Kiamos I., Shapon M., Strong S., Sun B.,

Shie B.C., Shen Y. Manner B.W., Khorley R., Wun D., Yang S., Yang S.,

Sheng X.H., Monded E.W., Rohn M., Shong S., Sun B.
HKAYKDKNKYRFEIMGEEEI--AFKMIRTNVSHVVGQLDDIRKNPRKFVCLNDNI-DHNH 230
                    RANFGKVPRYRYHVSAKIGIYSNFKWLISNITQVVDALDELRKTPKKFNCINDNLSDDRP 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426065; PubMed=12537568; Celniker S.W., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patels D.M., Park S., Speiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                        639 DDNQLIGALLEDFYLSLFPARSSFELESTYRNRFORYDDYRSW 681
                                                                    KDAQTVKAVLRDFYESMFPIPSQFELPREYRNRFLHMHELQEW 273
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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01-JUN-2003 (
01-MAR-2004 (
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                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 DIYSHSLIATNWLLNRAYGFKARHVLAHVGFLIDKDIVEAMQRRFHQQILDTAHQRFRAP
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Missa B., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Calniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J. K.S., Shuburner M., Gelbart W.M., Shu S.Q., Strapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
"Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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"Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IntAct; 09V553; -- IntAct; 09V553; -- G80027. FlyBase, FBgn0033392; CG8027. GO; 00:0016020; C:membrane; IEA. GO; GO:0030154; P:cell differentiation; IEA. InterPro; IPR00800; Notch_region.
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Matches 108, Conservative
                                                                                                                                                                                                                                                                                                     perspective.
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EMBL; X14814; CAA32919.1; -.

EMBL; X96722; CAA65494.1; -.

EMBL; X96722; CAA65494.1; -.

EMBL; Z71526; CAA96157.1; -.

EMBL; Z71526; CAA96157.1; -.

EMBL; 271526; CAA96157.1; -.

EMBL; 271526; CAA96157.1; -.

EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON EMBL; AMSON 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 KIHKAYKDKNKYRFEIMGEEEIAFKMIRTNVSHV----VGQLDDIRKNPRKFVC--LNDN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insequence analysis of the 33 kb long region between ORC5 and SU11 from "Sequence analysis of the 33 kb long region between ORC5 and SU11 from the left arm of chromosome XIV from Saccharcmyces cerevisiae.";
Yeast 13:849-860(1997).

-i- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mre11 complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mre11 by unwinding and/or repositioning DNA ends into the mre11 active site.
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                                                                                                                                         containing a
                                                                                                Alani E., Subbiah S., Kleckner N., "The yeast RAD50 gene encodes a predicted 153-kD protein contpurine nucleotide-binding domain and two large heptad-repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 1312;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
MEDLINE=97377992; PubMed=9234673;
Sen-Gupta M., Gueldener U., Beinhauer J.D., Fiedler T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65; Mismatches 126; Indels
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                                                                    MEDLINE=89276917; PubMed=2659437;
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617
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734
1312 AA;
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SEQUENCE FROM N.A.
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Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
A George R., Gonzalez M., Gurall H., Kromiller B., Li P., Liao G.,
A Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.
A Celniker S.,
Buttler S.,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AYO89618; AAL90356 1; -
R Flykase; Fegnon033392; CG802.
R Flykase; Fegnon03392; CG802.
R GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; Notch_region.
R Florerpro; IFR000800; Notch_region.
R Florerpro; PR000800; Notch_region.
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R Florerpro; PR000800; Notch_region.
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 14, Last amoutation update)
05-JUL-2004 (Rel. 44, Last amoutation update)
DNA repair protein RAD50 (153 KDa protein).
Name-FAD50; OrderedLocusNames-YNL250W; ORFNames=N0872;
Saccharomyces cerevisiae (Baker's yeast)
Eukaryote; Fungl; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
[1]
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                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Bphydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 29.2%; Score 506; DB 2; Length 666
Local Similarity 33.6%; Pred. No. 4e-29;
nes 108; Conservative 70; Mismatches 133; Indels
                                                                                                                Last sequence update)
Last annotation update)
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666 AA
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                                                                01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
RA50 YEAST
1D RA50 YEAST
AC P12753,
DT 01-0CT-1989
DT 01-0CT-1989
DT 05-JUL-2004
DE DNA repair p
GN Name=RAD50,
OS Saccharomyce
OC Bukaryota; F
OC Saccharomyce
OC Saccharomyce
OC Saccharomyce
OC Saccharomyce
OC NCBI_TAXID=4
RN [1]
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                                Q8SX14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4905;
                                                                                                                                                                                             05-JUL-2004
05-JUL-2004
05-JUL-2004
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01-JUN-2004
01-JUN-2004
                                                                                                                                                                                                                                                                                              Name=PDD4;
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Best Local S
Matches 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match
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                                                                                                   RESULT 13
                                                                                                                          QEJUT9
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fagle M., Anthouard V., Babour A., Barbe V.,
Goffard N., Frangeul L., Agie M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
A Wennene D., Tekaia F., Mesolowski-Louvel M. Westhof E., Wirth B.,
Zeniou-Mayer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souriet J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
: | : | | : | | EAGKETYEKORINHLSSLKE---AFQHKFQGLSNIENSDMAQVNHEMSQFKAFISQDLTDT 408
                                                                                                                          468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 FGDLESNAINIE-----TOLANI----TSYLDLEIKTYEEDKOOYGDVWTIVDARDVT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                        23 RKVPAH-------MPHMIDRIVMQELQDMFPEEFDKTSFHKVRHSEDMQFAFSY--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 KQDIYVLQHFVEPINLLNIQLDEELASFFEID-PQHIVNAHNKTKSFVTR-KELDVIGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LTGLEHMLINCSKMLPADITQLNNIPPTQESYYDPNLPPVTKS-----LVTNCKPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKIHKAYKDKNKY------RFEIMGEEEIAFKMIRTNVSHVVGQLDD-----I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida glabrata (Yeast) (Torulopsis glabrata).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 117.5; DB 2; Length
19.4%; Pred. No. 3.4;
ative 54; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; CR380958; CAG62218.1; -.
SEQUENCE 691 AA; 80473 MW; 12D26B88BD8BAABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to tr/Q12033 Saccharomyces cerevisiae YOR275c.
ORFNAMMes=CAGL10956g;
                                                                                                                                                                                                                                                                                                                                            691 AA
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                  SLNHELENLKTYKEKLOSW 487
                                                                                                                                                                        -- MHELQEWRAYRDKLKFW 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome evolution in yeasts.";
Nature 430:35-44(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5478;
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                                                                                                                        409
                                                                          226
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63 MQFAFSYFYYLMSAVQPLNISQVFDE-----VDTDQSGVLSDREIRTLATRIHELPLSL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 QSLQ-LDKIKSDLQAKHYQAMINNVNAKNKEQERTFRLYABEVKRELRNEMEV-DRLES 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 AYKDKNKYRFEIMGEEEIAFK------MIRTN-----VSHVVGQLDDIRKNPRK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 RISNMNKRRASPRDDABAEPKRQKFDNDRFLSLVKENSHLQHDLNKLVGVLLRLQKFLKS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVCLNDN-------FPIPS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 FGQLNSNSKVPSTFIPTDSELLAIDHHNFDLQKYDLILFDLLKPLNGDSIDDTFKFKKNN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 NAAQYVNQKLSAK-GYFSNK----PNKLRQLLLLSLDSSQLIPBNAENPEISEKVYEND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 DSLRYVNKILNSKFGFTSRKVPAHMPHMIDRIVMQEL--QDMFPEEFDKTSFHKVRHSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
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STRAIN=CB64732;
Monastyrska I., Kiel J.A.K.W., Veenhuis M.;
"The H. polymoxpha PDD4 gene product is required for selective peroxisome degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                              STRAIN=CBS4732;
Monastyrska I., Kiel J.A.K.W., Veenhuis M.;
Monastyrska I., Kiel J.A.K.W., Veenhuis M.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY304543; AAQV4772.1; -
SEQUENCE 384 AA; 45251 WW; E294618BBCE6AC12 CRC64;
                                                                         Last sequence update)
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Pred. No. 3.2;
2; Mismatches 130;
                                                                                                                                                                        Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota, Fungi, Ascomycota, Saccharomycotina,
Saccharomycetales, Saccharomycetaceae, Pichia.
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Bukaryota, Fungi, Ascomycota, Saccharomycotina;
Saccharomycetales, Saccharomycetaceae, Pichia.
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0, 4 0,	Query Match 6.6%; Score 113.5; DB 2; Length 384; Best Local Similarity 20.5%; Pred. No. 3.2; Matches 69; Conservative 62; Mismatches 130; Indels 75; Gaps 15;		63	112 RN-VMNIIYSLENSAEISKQFKETALKKWADKDABIBLLKNBVBKLNKKVDBKERNI 167	117 QDLTGLEHMLING-SKWLPADITQLNNIPPTQESYYDPNLPPYTKSLYTNCKPVTDKIHK 175	176 AYKDKNKYRFEIMGEBEIAFKMIRTNVSHVVGQLDDIRKNPRK 21	226 RLSNMNKRRASPRDDAEAEPKRQKFDNDRFLSLVKENSHLQHDLNKLVGVLLRLQKFLKS 285	219 FVCLNDNIDHNIKDAQTVKAVLRDFYBSMFPIPS 252	253 OFELPREYRNRFLHMHELOEWRAYR 277	: :	PRELIMINARY; PRT; 545 068215 068215 01-AUG-1998 (TrEMBLrel. 07, Last sequenc 01-AUG-1998 (TrEMBLrel. 07, Last sequenc 01-AUG-1998 (TrEMBLrel. 19; Last annotat SacB. Name=sacB; Name=sacB; Neisseria meningitidis (serogroup A). Bacteria; Proteobacteria; Betaproteobact NCBL_TAXID=65699; [1] SEQUENCE FROM N.A. STRAIN=F8229; SWARTLE-8917678; PubMed=9515923; SWARTLE-8917678; PubMed=9515923; SWARTLE-8917678; PubMed=9515923; SWARTLE-8917678; PubMed=9515923; SWARTLE-8917678; PubMed=9515923; SWARTLE-8017678; PubMed=9515923; SWARTLE-SOURCE 545 AJ; 64097 MW; 1BC3400C5 SEQUENCE 545 AJ; 64097 MW; 1BC3400C5 SEQUENCE 545 AJ; 64097 MW; 1BC3400C5 SEQUENCE 545 AJ; GOBSETVALINSKFGFTSKKVPAHMPHMI 3 FADSLRYVNKILNSKFGFTSKKVPAHMPHMI 3 FADSLRYVNKILNSKFGFTSKKVPAHMPHMI 3 SADSLRYVNKILNSKFGFTSKKVPAHMPHMI 3 SADSLRYVNKILNSKFGFTSKKVPAHMPHMI 3 SADSLRYVNKILNSKFGFTSKKVPAHMPHMI 3 SADSLRYVNKILNSKFGFTSKKPTKHTHSPGSM	455 IAVTGYLYHHYALLSGRALQSSBKTB 480 122 LEHMLINCSKMIPADITQLNNIPP-TQESYYDPNLPPVTKSLVTNCKPVTDKIHKAYKDK 180
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